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OM protein - protein search, using sw model

Run on: July 30, 2004, 11:14:51 ; Search time 47.9085 Seconds

(without alignments)
1433.128 Million cell updates/sec

Title: US-09-297-181-2

Perfect score: 1289

Sequence: 1 QVQLQSGAEIVRSAGSVKL.....CMQGTHSPITFGAGTKLEIK 243

Scoring table: BLOSUM62

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1289	100.0	243	2	AAM60769 Single ch
2	1277	99.1	535	2	AAM28491 Human p53
3	1277	99.1	535	2	AAM28492 Human p53
4	985.5	76.5	353	2	AAY06273 Anti Fc a
5	970.5	75.3	257	3	AAB09777 Antiviral
6	961	74.6	249	2	AAM60770 Single ch
7	930.5	72.2	238	5	AAM25963 KDR bindi
8	930.5	72.2	238	5	AAM25963 KDR bindi
9	930.5	72.2	238	6	AAM25963 KDR bindi
10	926.5	71.9	240	5	AAM25960 KDR bindi
11	926.5	71.9	240	5	AAM25960 KDR bindi
12	926.5	71.9	240	5	AAM25960 KDR bindi
13	920.5	71.4	253	5	ABP45953 Human Bly
14	918.5	71.3	238	5	ABP45953 KDR bindi
15	913	70.8	241	7	ADD31766 Anti-CEA
16	911	70.7	281	2	AAM82744 Fusion pr
17	911	70.7	281	2	AAM82744 Fusion pr
18	908	70.4	240	7	ADD31769 Anti-CEA
19	908	70.3	270	4	AAR75719 MFE-23 an
20	902	70.0	251	4	AAB70171 Recombina
21	902	70.0	556	4	AAM80040 SCFV-rear
22	902	70.0	556	4	AAM80040 SCFV-rear
23	900.5	69.9	271	3	AAB23818 Plasmid p
24	900.5	69.9	271	4	AAG67494 Amino aci
25	900.5	69.9	271	5	AAM47632 Murine MA

26	900.5	69.9	271	5	ABG97809 Mouse MAB
27	900.5	69.9	271	5	ABG35312 Thrombopo
28	900.5	69.9	274	3	AAB23817 Plasmid p
29	900.5	69.9	274	3	AAG67493 Amino aci
30	900.5	69.9	274	5	AAM47631 Murine MA
31	900.5	69.9	274	5	ABG97808 Mouse MAB
32	900.5	69.9	274	5	ABG35311 Thrombopo
33	900	69.8	553	2	AAM1508 Single ch
34	900	69.8	553	2	AAM1508 Single ch
35	900	69.8	553	4	AAB61960 Bispecific
36	900	69.8	553	4	AAB61960 Bispecific
37	895.5	69.5	249	1	AAP80154 Biosynthe
38	892.5	69.2	245	5	AAM47636 Murine MA
39	892.5	69.2	245	5	ABG97813 Mouse MAB
40	892.5	69.2	245	5	ABG35316 Thrombopo
41	892.5	69.2	271	3	AAB23820 Plasmid p
42	892.5	69.2	271	4	AAG67496 Amino aci
43	892.5	69.2	271	5	AAM47634 Murine MA
44	892.5	69.2	271	5	ABG97811 Mouse MAB
45	892.5	69.2	271	5	ABG97811 Mouse MAB

ALIGNMENTS

RESULT 1

AAM60769 standard; protein; 243 AA.

AAM60769;

08-SEP-1998 (first entry)

Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.

Single chain antibody; SCFV 421; mouse; p53 protein; oligomerisation;

regulatory domain; p53 mutant; H273; W248; G281;

p53-dependent trans-activating activity; restoration;

tumour-suppressing activity; tumour cell; treatment; hyper-proliferation;

cancer; re-stenosis; ss.

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Claim 5; Page 31; 54pp; French.

The present sequence represents a single chain antibody (ScFv) designated 421. The antibody binds to an epitope present in the C-terminal region of the p53 protein that includes oligomerisation and regulatory domains, specifically between positions 320 and 393. ScFv 421 is directed against p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is introduced into cells containing a mutant p53 protein, p53-dependent trans-activating activity is restored. ScFv 421 is specific for p53-mutants that have lost tumour-suppressing activity and are present in tumour cells. It is particularly used to treat hyper-proliferation

CC associated with these mutants (e.g. cancer and re-stenosis) but may also
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant
 CC and to purify or detect p53

XX Sequence 243 AA;

Query Match 100.0%; Score 1289; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1.3e-83;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGAEIVRSASVLTSLTASGFNPKDYMMHWKORPEQGLMIGWIDPENGDTXY 60
 DB 1 QVQLQSGAEIVRSASVLTSLTASGFNPKDYMMHWKORPEQGLMIGWIDPENGDTXY 60
 QY 61 APPEQKATMTADTSNTAVLQSLASBEDTAVVYCNFYGDALDYGQGTVTYVSSGGGG 120
 DB 61 APPEQKATMTADTSNTAVLQSLASBEDTAVVYCNFYGDALDYGQGTVTYVSSGGGG 120
 QY 121 SGGGSGGGGGSDVLMQTPLTSLTIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSP 180
 DB 121 SGGGSGGGGGSDVLMQTPLTSLTIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSP 180
 QY 181 KRLLIVSKLDSGVPPRFSGSGGTPETLKINVEAEDLGVIYCMQGTSPFTFGAGTKL 240
 DB 181 KRLLIVSKLDSGVPPRFSGSGGTPETLKINVEAEDLGVIYCMQGTSPFTFGAGTKL 240
 QY 241 EIK 243
 DB 241 EIK 243

RESULT 2

AAW28491
 ID AAW28491 standard; protein; 535 AA.

XX AAW28491;

DT 25-NOV-1997 (first entry)

XX Human p53 protein variant S-325 encoded by p53C176.

XX Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
 KW substitution; replacement; transactivation; viral protein VP16; HSV;
 KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
 KW tumour suppression; apoptosis; single chain antibody variable domain.

OS Homo sapiens.
 OS Herpes simplex virus.
 OS Synthetic.
 OS Chimeric.

XX WO9704092-A1.

XX 06-FEB-1997.

XX 17-JUL-1996; 96WO-FR001111.

XX 19-JUL-1995; 95FR-00008729.

XX (RHON) RHONE POULENC RORER SA.

XX Conseller E, Bracco L;

XX MPI; 1997-132633/12.

XX N-PSDB; AAT86221.

XX New p53 variants e.g. with oligomerisation domain replaced by leucine
 FT zipper - useful for treating hyper-proliferative disorders, esp. cancer
 PT and restenosis.

XX Claim 36; Page 88-90; 133pp; French.

XX Claimed variants of protein p53 have at least part of the oligomerisation

CC domain deleted and replaced by a leucine zipper domain. The mutants
 CC preferably also have at least part of the p53 transactivating domain
 CC (amino acids 1-74) deleted and replaced by the transactivating domain
 CC (TD) from herpes simplex virus viral protein VP16 (amino acids 411-490)
 CC or by a protein domain able to bind selectively to a transactivator.
 CC especially a single-chain antibody variable domain (ScFv). The present
 CC sequence is that of a specifically claimed p53 variant designated S-325
 CC and comprising a ScFv domain, amino acids 75-325 of human wild-type p53
 CC and a leucine zipper domain at the C-terminal. The p53 variants are more
 CC active and more stable tumour suppressors and apoptosis-inducing agents
 CC than wild-type p53 and are active where the wild-type protein is not,
 CC i.e. they are not inactivated by dominant negative or oncogenic mutants,
 CC nor by other cellular proteins (because the leucine zipper domain
 CC prevents formation of inactive mixed oligomers)

XX Sequence 535 AA;

Query Match 99.1%; Score 1277; DB 2; Length 535;
 Best Local Similarity 98.8%; Pred. No. 2.1e-82;
 Matches 240; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQSGAEIVRSASVLTSLTASGFNPKDYMMHWKORPEQGLMIGWIDPENGDTXY 60
 DB 3 QVQLQSGAEIVRSASVLTSLTASGFNPKDYMMHWKORPEQGLMIGWIDPENGDTXY 62
 QY 61 APPEQKATMTADTSNTAVLQSLASBEDTAVVYCNFYGDALDYGQGTVTYVSSGGGG 120
 DB 63 APPEQKATMTADTSNTAVLQSLASBEDTAVVYCNFYGDALDYGQGTVTYVSSGGGG 122
 QY 121 SGGGSGGGGGSDVLMQTPLTSLTIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSP 180
 DB 123 SGGGSGGGGGSDVLMQTPLTSLTIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSP 182
 QY 181 KRLLIVSKLDSGVPPRFSGSGGTPETLKINVEAEDLGVIYCMQGTSPFTFGAGTKL 240
 DB 183 KRLLIVSKLDSGVPPRFSGSGGTPETLKINVEAEDLGVIYCMQGTSPFTFGAGTKL 242
 QY 241 EIK 243
 DB 243 EIK 245

RESULT 3

AAW28492
 ID AAW28492 standard; protein; 535 AA.

XX AAW28492;

DT 25-NOV-1997 (first entry)

XX Human p53 protein variant S-325H.

XX Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
 KW substitution; replacement; transactivation; viral protein VP16; HSV;
 KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
 KW tumour suppression; apoptosis; single chain antibody variable domain.

OS Homo sapiens.
 OS Herpes simplex virus.
 OS Synthetic.
 OS Chimeric.

XX Key Location/Qualifiers

FT Misc-difference 361

XX WO9704092-A1.

XX 06-FEB-1997.

XX 17-JUL-1996; 96WO-FR001111.

XX

/note= "Arg residue at position 182 of wild-type p53 has
 been mutated to His"


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DB 158 VSAGGGGGGGGGGGGGVVTGTPPLTSLITIGQPASISCKSSQSGLDSDKTYLNMLL 217
QY 174 QRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKINRVEADLGVYTCWQGTISPLT 233
DB 218 QRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKINRVEADLGVYTCWQGTISPLT 277
QY 234 FGAGTYLEIK 243
DB 278 FGAGTYLEIK 287

RESULT 5
AAB09777
ID AAB09777 standard; protein; 257 AA.
AC AAB09777;
DE 06-SEP-2000 (first entry)
XX Anti-viral scFv-antibody against the 3a movement protein of CMV.
XX Molecular pathogenicity; plant disease; resistance; antibody; scFv;
XX gene construct; pathogen; toxin; fusion protein; antimicrobial;
XX deoxyribonuclease; RNase; ribosome inactivator; immunomodulator.
XX Tobacco mosaic virus.
XX Human herpesvirus 5.
XX WO200023593-A2.
XX 27-APR-2000.
XX 15-OCT-1999; 99WO-EP007844.
XX 16-OCT-1998; 98EP-00119630.
XX 16-OCT-1998; 98IN-MU000666.
XX (FRAU) FRAUNHOFER GES FORBILDUNG ANGEWANDTEN.
XX Fraeher R, Schillberg S, Naehring J, Sack M, Monecke M, Liao Y,
XX Spiegel H, Zimmermann S, Emons N, Holzem A;
XX WPI; 2000-339692/29.
XX New fusion proteins and gene constructs for expressing agents
XX (antibodies, enzymes, vectors or molecular pathogenicity), useful for
XX protecting plants against pathogens and increasing resistance to disease.
XX Example 6; Fig 23a; 193pp; English.
XX The present invention describes a fusion protein (I) comprising at least
XX one binding domain specifically recognising an epitope of a plant
XX pathogen and at least one further domain comprising a protein or peptide
XX sequence which is toxic to the pathogen or detrimental to its
XX replication, transmission or life cycle. Also described is a
XX pathogenicity (II) comprising (I) and a cellular targeting sequence
XX anchoring or at least one binding domain that specifically recognises a
XX viral movement and/or replicase protein. The fusion protein,
XX pathogenicity (II), polynucleotide, vectors, and compositions from the present
XX invention are useful for the protection of a plant against the action of
XX a pathogen. The kit from the present invention is useful for carrying out
XX the methods and may be employed in different applications, for example in
XX the diagnostic field or as research tools. The kit or its components,
XX such as the fusion protein, pathogenicity, polynucleotides, vectors or
XX compositions are useful in plant cell and plant tissue culture, in
XX agriculture. They are extremely useful for breeding new varieties of
XX plants that display improved properties such as resistance to pathogens.
XX AA056587 to AA056702 and AAB09774 to B097820 represent sequences used in
XX the exemplification of the present invention
XX Sequence 257 AA;
SQ

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Query Match 75.3%; Score 970.5; DB 3; Length 257;
Best Local Similarity 77.2%; Pred. No. Se-61;
Matches 193; Conservative 13; Mismatches 33; Indels 11; Gaps 3;

QY 1 QYOLQSGAEIVRSASVSLCTASGFNFKDYMEWVKQRPQGLEMTGIDPENGDTLEY 60
DB 3 EYQLOQSGAEIVRSASVSLCTASGFNFKDYMEWVKQRPQGLEMTGIDPENGDTLEY 62
QY 61 APRFOGKATMTDTSNTNRYLDLSSLASHTDIAVYVCNFFGADLADYWGQGTIVTSAGG- 119
DB 63 NQKFKGKATLTADKSSITAYWQISLTSDDSAVYVC---APPDVGACTLLITVSAAGAP 118
QY 120 ---GSG---GGSGGGGGDVLTMTQPLTSLITIGQPASISCKSSQSGLDSDKTYLNMLL 173
DB 119 TSGSGKPGPGESGTYKAPVYLTQAPLITSLVITIGQPASISCKSSQSGLDSDKTYLNMLL 178
QY 174 QRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKINRVEADLGVYTCWQGTISPLT 233
DB 179 QRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKINRVEADLGVYTCWQGTISPLT 238
QY 234 FGAGTYLEIK 243
DB 239 FGAGTYLEIK 248

RESULT 6
AAM60770
ID AAM60770 standard; protein; 249 AA.
AC AAM60770;
DE 08-SEP-1998 (first entry)
XX Single chain antibody (ScFv) D3M that binds to mutant p53 proteins.
XX Single chain antibody; scFv D3M; mouse; p53 protein; oligomerisation;
XX regulatory domain; p53 mutant; H273; W248; G281;
XX p53-dependent trans-activating activity; restoration;
XX tumour-suppressing activity; tumour cell; treatment; hyper-proliferation;
XX cancer; re-stenosis; ss.
XX Mus sp.
XX WO9818625-A1.
XX 07-MAY-1998.
XX 27-OCT-1997; 97WO-FR001921.
XX 29-OCT-1996; 96FR-00013176.
XX (RHON) RHONE-POULENC RORER SA.
XX Bracco L, Debussche J;
XX WPI; 1998-272140/24.
XX N-FSDB; AAV36237.
XX Restoring p53-dependent trans-activating activity to cell containing
XX mutant p53 - by delivering single-chain antibody specific for the mutant,
XX particularly for treatment of tumours.
XX Claim 5; Page 32; 54pp; French.
XX The present sequence represents a single chain antibody (ScFv) designated
XX D3M. The antibody binds to an epitope present in the C-terminal region of
XX the p53 protein that includes oligomerisation and regulatory domains,
XX specifically between positions 320 and 393. ScFv D3M is directed against
XX p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is
XX introduced into cells containing a mutant p53 protein, p53-dependent
XX trans-activating activity is restored. ScFv D3M is specific for p53-
XX mutants that have lost tumour-suppressing activity and are present in
CC

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CC tumour cells. It is particularly used to treat hyper-proliferation
 CC associated with these mutants (e.g. cancer and re-stenosis) but may also
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant
 CC and to purify or detect p53
 XX
 SQ Sequence 249 AA;

Query Match 74.6%; Score 961; DB 2; Length 249;
 Best Local Similarity 74.8%; Pred. No. 2.3e-60;
 Matches 187; Conservative 23; Mismatches 32; Indels 8; Gaps 3;

QY 1 QVQLQSGAEIVRSGASVSKLSTAGSPNIDKYMHVWKQRPQGLEWIGIDPENGDTXY 60
 D 1 QVQLQSGAEIVRSGASVSKLSTAGSPNIDKYMHVWKQRPQGLEWIGIDPENGDTXY 60
 QY 61 APRFQKATMTADTSSNTAVYLTQSLASEDTAVYYCN-----FYGDALDYMGGQTTVTV 114
 D 61 APRFQKATMTADTSSNTAVYLTQSLASEDTAVYYCN-----FYGDALDYMGGQTTVTV 120
 QY 115 SSGGGSGSGGGSGGSDVMTQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLNMLL 173
 D 121 SSGGGSGSGGGSGGSDVMTQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLNMLL 180
 QY 174 QRGSGPKRLIYVSLDGVPRFTGSGSDTFTLKINRVEADLGVYYCWGTHSPILT 233
 D 181 QRGSGPKRLIYVSLDGVPRFTGSGSDTFTLKINRVEADLGVYYCWGTHSPILT 239
 QY 234 FGAGTLEIK 243
 D 240 FGAGTLEIK 249

RESULT 7
 AAE25963
 ID AAE25963 standard; protein; 238 AA.
 AC AAE25963;

DT 15-NOV-2002 (first entry)
 DE KDR binding immunoglobulin related mouse protein #3.

KM Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;
 KM foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;
 KM VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;
 KW PIC11; scFv antibody.

OS Mus sp.

PN US2002064528-A1.

PD 30-MAY-2002.

PF 12-OCT-2001; 2001US-00976787.

PR 28-JAN-2000; 2000US-00493539.

PA (ZHUZ/) ZHU Z.

PA (WITT/) WITTE L.

PI Zhu Z, Witte L;

DR WPI; 2002-589175/63.

XX Novel immunoglobulin molecule for reducing tumor growth, binds to kinase
 XX insert domain-containing receptor with an affinity comparable to human
 XX vascular endothelial growth factor, and neutralizes activation of KDR.

PS Disclosure; Page 17-18; 34pp; English.

CC The present invention relates to novel immunoglobulin molecules that bind
 CC to kinase insert domain-containing receptor (KDR) (a human homologue of
 CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable

CC to human vascular endothelial growth factor (VEGF) and that neutralises
 CC activation of KDR. Sequences of the invention are useful for neutralising
 CC the activation of KDR, for reducing tumour growth and for inhibiting
 CC angiogenesis. The present sequence is KDR binding immunoglobulin related
 CC mouse protein
 XX
 SQ Sequence 238 AA;

Query Match 72.2%; Score 930.5; DB 5; Length 238;
 Best Local Similarity 71.7%; Pred. No. 3.1e-58;
 Matches 175; Conservative 27; Mismatches 35; Indels 7; Gaps 2;

QY 1 QVQLQSGAEIVRSGASVSKLSTAGSPNIDKYMHVWKQRPQGLEWIGIDPENGDTXY 60
 D 1 QVQLQSGAEIVRSGASVSKLSTAGSPNIDKYMHVWKQRPQGLEWIGIDPENGDTXY 60
 QY 61 APRFQKATMTADTSSNTAVYLTQSLASEDTAVYYCN-----FYGDALDYMGGQTTVTV 119
 D 61 APRFQKATMTADTSSNTAVYLTQSLASEDTAVYYCN-----FYGDALDYMGGQTTVTV 120
 QY 120 GSGGGSGSGGGSGGSDVMTQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLNMLLORPGQS 179
 D 121 GSGGGSGSGGGSGGSDVMTQTPLTSLVITIGQPASISCKSSQSLDSDGKTYLNMLLORPGQS 174
 QY 180 PKRLIYVSLDGVPRFTGSGSDTFTLKINRVEADLGVYYCWGTHSPILTFGAGTK 239
 D 175 PKRLIYVSLDGVPRFTGSGSDTFTLKINRVEADLGVYYCWGTHSPILTFGAGTK 234
 QY 240 LEIK 243
 D 235 LEIK 238

RESULT 8
 AAU74420
 ID AAU74420 standard; protein; 238 AA.
 AC AAU74420;

DT 26-MAR-2002 (first entry)

DE Antigen-binding protein, single chain variable fragment version #2.

KM Antigen-binding protein, single chain variable fragment; svFv; antigen;
 KM cytosolic; angiogenesis inhibitor; tumour; leukaemia; antibody;
 KM vascular endothelial growth factor receptor; VEGF;
 KW cell proliferation inhibitor.

OS Mus sp.

OS Synthetic.

PH Key Location/Qualifiers

FT Region 1..117

FT /label= VH

FT /note= "Heavy chain variable domain. Specifically claimed

FT in claim 61"

FT Region 118..132

FT /label= Linker

FT /note= "15 amino acid linker joins the VH and VL regions

FT of the single chain variable fragment protein. Encoded by

FT AAS20285"

FT Region 133..238

FT /label= VL

FT /note= "Light chain variable domain. Specifically claimed

FT in claim 61"

PN WO200190192-A2.

PD 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US016924.

PR 24-MAY-2000; 2000US-0206749P.

XX (IMCL-) IMCLONE SYSTEMS INC.
PA
XX
XX

Zhu Z;
PI

WPI; 2002-106189/14.
DR

New bispecific immunoglobulin-like antigen-binding protein for reducing tumor growth and for inhibiting angiogenesis, comprises a complex of two polypeptides and two second polypeptides.
PT
PT

Claim 63; Page 62-63; 64pp; English.
PS

XX The invention describes an antigen-binding protein (I) comprising a
XX complex of two polypeptides (P1) and two second polypeptides (P2) which
XX are stably associated in an immunoglobulin like complex. P1 has an
XX antigen-binding site located to the N terminus of immunoglobulin (Ig)
XX light chain constant domain (CL domain), and P2 has an antigen-binding
XX site located to the N terminus of the CH1 domain. (I) is useful for:
XX neutralising the activation of a vascular endothelial growth factor
XX (VEGF) receptor; reducing tumour growth; inhibiting VEGF induced
XX reducing endothelial cell proliferation; blocking interaction of a protein and
XX migration of human leukaemia cells; blocking interaction of a protein and
XX its ligand; promoting interactions between immune cells and target cells;
XX and in vivo and in vitro for investigative, diagnostic or treatment
XX methods. The design of (I) provides for efficient production so that
XX substantially all of the antigen-binding proteins produced are assembled
XX in the desired configuration. (I) is bivalent and bispecific, homogeneous
XX and in retimeric form. The heavy chain constant domains which constitute
XX the re region (e.g., CH2 and CH3 for an Ig molecule) of a natural
XX antibody and which provide other antibody functions can be present. There
XX is no requirement for processing in vitro to obtain the complete product.
XX This is the amino acid sequence of a single chain variable fragment
XX (scFv), an engineered protein containing a variable light and variable
XX heavy domain on one polypeptide, described in the method of the invention
XX
SQ Sequence 238 AA;

Query Match 72.2%; Score 930.5; DB 5; Length 238;

Best Local Similarity 71.7%; Pred. No. 3.1e-58;
Matches 175; Conservative 27; Mismatches 35; Indels 7; Gaps 2;

```
QY 1 QVQLQSGAEIVSGASVKLSCTASGPNIKDYHWMVKORPEGLEWIGIDPENGDTTEY 60
DB 1 QVQLQSGAEIVSGASVKLSCTASGPNIKDYHWMVKORPEGLEWIGIDPENGSDY 60
QY 61 APRFOGKATMTADSSNTAYQLSLASEDTAVYYCN-FYGDALDYMGGTTVTVSSGGG 119
DB 61 APRFOGKATMTADSSNTAYQLSLASEDTAVYYCNAYGDYDYGWGGTTVTVSSGGG 120
QY 120 GSGGGSGGGSDVLMQTPLTSLVTIGOPASISCKSSQSLDSDGKTYLWMLQRPQS 179
DB 121 GSGGGSGGGSDIRLTQSPALMSAPGKVTITCSASSV-----SYMFMFOQKPTGS 174
QY 180 PKRLIYWSKIDSGVPDRFPTSGSGDTFTLKINRVEADLVGYVYCWGCTHSPITFGAGT 239
DB 175 PKLMTYSTNLASGVPAFPGSSGSGTSTLTISRVEADATVYCOQRRSYPTFTGSGTK 234
QY 240 LEIK 243
DB 235 LEIK 238
```

RESULT 9

ABJ26732
ID ABJ26732 standard; protein; 238 AA.

ABJ26732;
AC

01-MAY-2003 (first entry)
DT

VEGF binding related protein SEQ ID No 28.
XX
XX
DE
XX

KW Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;
KM leukaemia cell; vascular endothelial growth factor; tumour;
XX bispecific antigen-binding protein; mouse; murine.
XX

Mus sp.
OS

WO2003002144-A1.
XX

09-JAN-2003.
XX

26-JUN-2002; 2002W0-US020332.
XX

26-JUN-2001; 2001US-0301299P.
XX

(IMCL-) IMCLONE SYSTEMS INC.
XX

Zhu Z;
PI

WPI; 2003-201468/19.
DR

XX New bispecific antibodies having antigen-binding sites specific for a
XX first vascular endothelial growth factor (VEGF) receptor and for a second
XX VEGF receptor, useful for inhibiting migration of leukemia cells, or for
XX treating tumors.
XX
XX

Disclosure; Page 56-57; 98pp; English.
PS

XX The invention relates to a novel antibody having a first antigen binding
XX site specific for a first vascular endothelial growth factor (VEGF)
XX receptor and a second antigen-binding site specific for a second VEGF
XX receptor. The bispecific antigen-binding proteins block activation of the
XX VEGF receptor and are useful for reducing or inhibiting VEGF-induced
XX cellular functions such as mitogenesis of vascular endothelial cells and
XX migration of leukaemia cells. The antibodies are useful for treating
XX tumours and for in vivo or in vitro for investigative and diagnostic
XX methods. This sequence represents a mouse protein relating to the
XX bispecific antibodies that bind to the VEGF receptors of the invention
XX
SQ Sequence 238 AA;

Query Match 72.2%; Score 930.5; DB 6; Length 238;

Best Local Similarity 71.7%; Pred. No. 3.1e-58;
Matches 175; Conservative 27; Mismatches 35; Indels 7; Gaps 2;

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QY 1 QVQLQSGAEIVSGASVKLSCTASGPNIKDYHWMVKORPEGLEWIGIDPENGDTTEY 60
DB 1 QVQLQSGAEIVSGASVKLSCTASGPNIKDYHWMVKORPEGLEWIGIDPENGSDY 60
QY 61 APRFOGKATMTADSSNTAYQLSLASEDTAVYYCN-FYGDALDYMGGTTVTVSSGGG 119
DB 61 APRFOGKATMTADSSNTAYQLSLASEDTAVYYCNAYGDYDYGWGGTTVTVSSGGG 120
QY 120 GSGGGSGGGSDVLMQTPLTSLVTIGOPASISCKSSQSLDSDGKTYLWMLQRPQS 179
DB 121 GSGGGSGGGSDIRLTQSPALMSAPGKVTITCSASSV-----SYMFMFOQKPTGS 174
QY 180 PKRLIYWSKIDSGVPDRFPTSGSGDTFTLKINRVEADLVGYVYCWGCTHSPITFGAGT 239
DB 175 PKLMTYSTNLASGVPAFPGSSGSGTSTLTISRVEADATVYCOQRRSYPTFTGSGTK 234
QY 240 LEIK 243
DB 235 LEIK 238
```

RESULT 10

AAE25960
ID AAE25960 standard; protein; 240 AA.

AAE25960;
AC

15-NOV-2002 (first entry)
DT

XX
XX

[illegible]

DT	26-MAR-2002 (first entry)	
XX		
DE	Antigen-binding protein, single chain variable fragment version #1.	
XX		
KW	Antigen-binding protein; single chain variable fragment; scFv; antigen;	
KM	cytostatic; angiogenesis inhibitor; tumour; leukaemia; antibody;	
KW	vascular endothelial growth factor receptor; VEGF;	
KM	cell proliferation inhibitor.	
XX		
OS	Mus sp.	
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Region	1..117
FT		/label= VH
FT		/note="Heavy chain variable domain. Specifically claimed
FT		in claim 57"
FT	Region	118..132
FT		/label= Linker
FT		/note="15 amino acid linker joins the VH and VL regions
FT		of the single chain variable fragment protein. Encoded by
FT		AAS20285"
FT	Region	133..240
FT		/label= VL
FT		/note="Light chain variable domain. Specifically claimed
FT		in claim 57"
XX		
XX		
PN	WO200190192-A2.	
XX		
PD	29-NOV-2001.	
XX		
XX		
PF	24-MAY-2001; 2001WO-US016924.	
XX		
PR	24-MAY-2000; 2000US-0206749P.	
XX		
PA	(IMCL-) IMCLONE SYSTEMS INC.	
XX		
PI	Zhu Z;	
XX		
XX	WPI; 2002-106189/14.	
XX		
PT	New bispecific immunoglobulin-like antigen-binding protein for reducing	
PT	tumor growth and for inhibiting angiogenesis, comprises a complex of two	
PT	polypeptides and two second polypeptides.	
XX		
PS	Claim 63; Page 62; 64pp; English.	
XX		
CC	The invention describes an antigen-binding protein (1) comprising a	
CC	complex of two polypeptides (P1) and two second polypeptides (P2) which	
CC	are stably associated in an immunoglobulin like complex. P1 has an	
CC	antigen-binding site located to the N terminus of immunoglobulin (Ig)	
CC	light-chain constant domain (CL domain), and P2 has an antigen-binding	
CC	site located to the N terminus of the CH1 domain. (1) is useful for:	
CC	neutralising the activation of a vascular endothelial growth factor	
CC	(VEGF) receptor; reducing tumour growth; inhibiting angiogenesis;	
CC	reducing endothelial cell proliferation; inhibiting VEGF induced	
CC	migration of human leukaemia cells; blocking interaction of a protein and	
CC	its ligand; promoting interactions between immune cells and target cells;	
CC	and in vivo and in vitro for investigative, diagnostic or treatment	
CC	methods. The design of (1) provides for efficient production so that	
CC	substantially all of the antigen-binding proteins produced are assembled	
CC	in the desired configuration. (1) is bivalent and bispecific, homogeneous	
CC	and in tetrameric form. The heavy chain constant domains which constitute	
CC	the FC region (e.g., CH2 and CH3 for an IgG molecule) of a natural	
CC	antibody and which provide other antibody functions can be present. There	
CC	is no requirement for processing in vitro to obtain the complete product.	
CC	(scFv), an engineered protein containing a variable light and variable	
CC	heavy domain on one polypeptide, described in the method of the invention	
XX		
XX	Sequence 240 AA;	
XX		

Query Match
71.9%; Score 926.5; DB 5; Length 240;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2004, 11:17:36 ; Search time 14.3232 Seconds
(without alignments)
875.861 Million cell updates/sec

Title: US-09-297-181-2

Perfect score: 1289

Sequence: 1 QVQLQSGAEIVSGASVKL.....CMQGTSPILTFAGTKLEIK 243

Scoring table:

BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1277	99.1	535	US-08-983-035A-38	Sequence 38, Appl
2	985.5	76.5	353	US-09-203-958A-4	Sequence 4, Appl
3	911	70.7	281	US-09-423-439-44	Sequence 44, Appl
4	911	70.7	666	US-09-423-439-51	Sequence 51, Appl
5	906	70.3	270	US-08-652-507-2	Sequence 2, Appl
6	900	69.8	553	US-08-661-052-16	Sequence 16, Appl
7	900	69.8	553	US-08-188-082-16	Sequence 16, Appl
8	900	69.8	553	US-09-364-088-16	Sequence 16, Appl
9	900	69.8	553	US-09-102-716-16	Sequence 16, Appl
10	866	67.2	348	US-09-646-028-12	Sequence 12, Appl
11	866	67.2	361	US-09-646-028-14	Sequence 14, Appl
12	843.5	65.4	288	US-09-423-439-38	Sequence 38, Appl
13	843.5	65.4	288	US-09-184-658-63	Sequence 63, Appl
14	843.5	65.4	289	US-09-504-262D-63	Sequence 63, Appl
15	843.5	65.4	673	US-09-423-439-32	Sequence 32, Appl
16	829	64.3	248	US-09-649-063-23	Sequence 23, Appl
17	828.5	64.3	247	US-09-227-693-34	Sequence 34, Appl
18	828.5	64.3	248	US-08-331-398A-34	Sequence 34, Appl
19	828.5	64.3	248	US-08-331-397B-34	Sequence 34, Appl
20	828.5	64.3	248	US-08-759-804A-34	Sequence 34, Appl
21	815.5	63.0	281	US-08-025-769B-178	Sequence 178, Appl
22	812	63.0	365	US-08-875-811-53	Sequence 53, Appl
23	812	63.0	366	US-08-875-811-55	Sequence 53, Appl
24	809.5	62.8	269	US-09-070-408-132	Sequence 132, Appl
25	804	62.4	239	US-08-279-772A-8	Sequence 8, Appl
26	804	62.4	239	US-08-902-486-11	Sequence 11, Appl
27	804	62.4	599	US-08-463-163-3	Sequence 3, Appl

28	801.5	62.2	263	US-08-752-844-66	Sequence 66, Appl
29	801.5	62.2	263	US-09-293-533-66	Sequence 66, Appl
30	798.5	61.9	260	US-08-447-402-1	Sequence 1, Appl
31	798	61.9	240	US-10-092-246-36	Sequence 36, Appl
32	795.5	61.7	240	US-10-092-246-37	Sequence 37, Appl
33	795.5	61.7	246	US-08-257-341-7	Sequence 7, Appl
34	795.5	61.7	252	US-08-133-804-4	Sequence 4, Appl
35	795.5	61.7	252	US-08-461-838-4	Sequence 4, Appl
36	795.5	61.7	252	US-08-461-886-4	Sequence 4, Appl
37	795.5	61.7	367	US-08-257-341-5	Sequence 5, Appl
38	791.5	61.4	244	US-09-244-369B-1	Sequence 1, Appl
39	785	60.9	269	US-08-646-265A-109	Sequence 109, Appl
40	784	60.8	240	US-10-092-246-35	Sequence 35, Appl
41	780.5	60.6	268	US-09-554-765-2	Sequence 2, Appl
42	780.5	60.6	268	US-09-554-765-15	Sequence 15, Appl
43	780.5	60.6	409	US-09-554-765-14	Sequence 14, Appl
44	776.5	60.2	249	US-08-797-689-18	Sequence 18, Appl
45	776.5	60.2	249	US-09-984-186-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-983-035A-38
Sequence 38, Application US/08983035A
Patent No. 6326464
GENERAL INFORMATION:
APPLICANT: CONSEILLER, EMMANUEL
BRACCO, LAURENT
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
USERS THEREOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARROW, GARRETT &
DONNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983, 035A
FILING DATE: 20-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/01111
FILING DATE: 17-JUL-1996
APPLICATION NUMBER: FR 95/08729
FILING DATE: 19-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Strauss, William L.
REGISTRATION NUMBER: 47,114
REFERENCE/DOCKET NUMBER: 03804, 0142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-08-983-035A-38
Query Match 99.1%; Score 1277; DB 4; Length 535;
Best local Similarity 98.8%; Pred. No. 6, 8e-95;

Matches 240; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLQSGAEIVRSGASVYKLSCTASGFNIKIDYMHMWKQREPGGLEWIGWIDPENGDTLEY 60
Db 3 QVQLQSGAEIVRSGASVYKLSCTASGFNIKIDYMHMWKQREPGGLEWIGWIDPENGDTLEY 62

QY 61 APRKQGRATMTADPSSNTAYIQLSLSASEDTAVYYCNFYGALDYWGQGTIVTVSSGGGG 120
Db 63 APRKQGRATMTADPSSNTAYIQLSLSASEDTAVYYCNFYGALDYWGQGTIVTVSSGGGG 122

QY 121 SGGGSGGGGSDVMTQPTLTSLVTIGQPASISCKSSQSLSDSDGKTYLNLQRPQSP 180
Db 123 SGGGSGGGGSDVMTQPTLTSLVTIGQPASISCKSSQSLSDSDGKTYLNLQRPQSP 182

QY 181 KRLIYVSKLDSGVDPDRFTSGSGSDTFTLKINRYEADLGVYYCWMQGTHTSPFTGAGTKL 240
Db 183 KRLIYVSKLDSGVDPDRFTSGSGSDTFTLKINRYEADLGVYYCWMQGTHTSPFTGAGTKL 242

QY 241 EIK 243
Db 243 EIK 245

RESULT 2
US-09-203-958A-4
Sequence 4, Application US/09203958A
Patent No. 6682928
GENERAL INFORMATION:
APPLICANT: KELLER, Tibor
APPLICANT: GOLDSTEIN, Joel
APPLICANT: GRAZIANO, Robert
APPLICANT: DEO, Yashwant M.
TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
FILE REFERENCE: MXI-099CPA
CURRENT APPLICATION NUMBER: US/09/203,958A
CURRENT FILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 60/067232
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 353
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-09-203-958A-4

Query Match 76.5%; Score 985.5; DB 4; Length 353;
Best Local Similarity 75.2%; Pred. No. 1.1e-71;
Matches 188; Conservative 23; Mismatches 32; Indels 7; Gaps 2;

QY 1 QVQLQSGAEIVRSGASVYKLSCTASGFNIKIDYMHMWKQREPGGLEWIGWIDPENGDTLEY 60
Db 38 EIQQLQTEPELVKPKASVYKISGASGFTDYIIPWQSHKLEWVGNNPPYGSTSY 97

QY 61 APRKQGRATMTADPSSNTAYIQLSLSASEDTAVYYC---NFYG---DALDYWGQGTIVT 113
Db 98 NIKFKGKATLTIVDKSSSTAYVQNLNLSDEDSAVYYCVAGVYYVGGSYEAFPWGGTIVT 157

QY 114 VSSGGSGGGGSDVMTQPTLTSLVTIGQPASISCKSSQSLSDSDGKTYLNLQRP 173
Db 158 VSAAGSGGGGSDVMTQPTLTSLVTIGQPASISCKSSQSLSDSDGKTYLNLQRP 217

QY 174 QRPQSPKRLIYVSKLDSGVDPDRFTSGSGSDTFTLKINRYEADLGVYYCWMQGTHTSP 233
Db 218 QRPQSPKRLIYVSKLDSGVDPDRFTSGSGSDTFTLKINRYEADLGVYYCWMQGTHTSP 277

QY 234 FGAGTKLEIK 243
Db 278 FGAGTKLEIK 287

RESULT 3
US-09-423-439-44
Sequence 44, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
APPLICANT: BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 09-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-423-439-44

Query Match 70.7%; Score 911; DB 4; Length 281;
Best Local Similarity 70.4%; Pred. No. 8.3e-66;
Matches 174; Conservative 27; Mismatches 36; Indels 10; Gaps 3;

QY 1 QVQLQSGAEIVRSGASVYKLSCTASGFNIKIDYMHMWKQREPGGLEWIGWIDPENGDTLEY 60
Db 23 EVQLQSGAEIVRSGASVYKLSCTASGFNIKIDYMHMWKQREPGGLEWIGWIDPENGDTLEY 82

QY 61 APRKQGRATMTADPSSNTAYIQLSLSASEDTAVYYCN--FYGD--ALDYWGQGTIVTVSS 116
Db 83 APRKQGRATMTADPSSNTAYIHLSLSASEDTAVYYCHVLIAGLIAMDYWGQGTIVTVSS 142

QY 117 GGGGSGGGGSDVMTQPTLTSLVTIGQPASISCKSSQSLSDSDGKTYLNLQRP 176
Db 143 GGGGSGGGGSDVMTQPTLTSLVTIGQPASISCKSSQSLSDSDGKTYLNLQRP 196

QY 177 GQSPKRLIYVSKLDSGVDPDRFTSGSGSDTFTLKINRYEADLGVYYCWMQGTHTSP 236
Db 197 GTSPEKRLIYVSKLDSGVDPDRFTSGSGSDTFTLKINRYEADLGVYYCWMQGTHTSP 256

QY 237 GTKLEIK 243
Db 257 GTKLEIK 263

RESULT 4
US-09-423-439-51
Sequence 51, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
APPLICANT: BLAKEY, David Charles

```

/ TITLE OF INVENTION: CHEMICAL COMPOUNDS
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Pillsbury Winthrop, L.L.P.
/ STREET: 1100 New York Ave., N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: MS Word
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/423 439
/ FILING DATE: 09-NO. 6339070-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GH98/01294
/ FILING DATE: 05-MAY-1998
/ APPLICATION NUMBER: GB 9709421.3
/ FILING DATE: 10-MAY-1997
/ INFORMATION FOR SEQ ID NO: 51:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 666 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-423-439-51

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Query Match          70.7%; Score 911; DB 4; Length 666;
Best Local Similarity 70.4%; Pred. No. 2,2e-65;
Matches 174; Conservative 27; Mismatches 36; Indels 10; Gaps 3;

QY 1 QVQLQSGAEIVRSASVSLCTASGFNIDKYYMHVWKORPEQGLFWMIGMIDPENDTXY 60
DB 20 EVQLQSGAEIVRSASVSLCTASGFNIDKNTMHVWKORPEQGLFWMIGMIDPENDTXY 79
QY 61 APFQKATMTADTSNTAYLQLSLTASEDTAVYYCN--FYGD--ALDYWGQGTIVT 116
DB 80 APFQKATMTADTSNTAYLQLSLTASEDTAVYYCHVLIVAGYLAAMDYWGQGTIVAVSS 139
QY 117 GGGSGSGGGSGGSGSVMTQTPLTISVTIGQPASISCKSSQSLDSDGKTYINMLLQRP 176
DB 140 GGGSGSGGGSGGSGSVMTQTPLTISVTIGQPASISCKSSQSLDSDGKTYINMLLQRP 193
QY 177 GQSPKRLIYVSKLDSGVDPDRFTGSGSDTFTLKINRVAEDLGVYYCWOGTHTSPITFGA 236
DB 194 GTSPKMIWYSTNLSAGVAPRFGSGSGTSTISITRMALDAATYYCCQRRSTYPLTFGA 253
QY 237 GTKLEIK 243
DB 254 GTKLEIK 260

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RESULT 5
US-08-652-507-2
/ Sequence 2, Application US/08652507
/ Patent No. 5876691
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Nixon & Vanderhye, P.C.
/ STREET: 1100 No. 5876691th Glebe Road, 8th floor
/ CITY: Arlington
/ STATE: Virginia
/ COUNTRY: USA

```

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/ ZIP: 22201-4714
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/652,507
/ FILING DATE: 02-JUL-1996
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Arthur R. Crawford
/ REGISTRATION NUMBER: 25,327
/ REFERENCE/DOCKET NUMBER: 117-211
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 703-816-4000
/ TELEFAX: 703-816-4100
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 270 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-652-507-2

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Query Match          70.3%; Score 906; DB 2; Length 270;
Best Local Similarity 69.2%; Pred. No. 2e-65;
Matches 173; Conservative 26; Mismatches 35; Indels 16; Gaps 3;

QY 1 QVQLQSGAEIVRSASVSLCTASGFNIDKYYMHVWKORPEQGLFWMIGMIDPENDTXY 60
DB 27 QVQLQSGAEIVRSASVSLCTASGFNIDKSYMHVWKORPEQGLFWMIGMIDPENDTXY 86
QY 61 APFQKATMTADTSNTAYLQLSLTASEDTAVYYCN-----FYGDALDYWGQGTIVT 113
DB 87 APFQKATMTADTSNTAYLQLSLTASEDTAVYYCNEGTPGPGY---FDYWGQGTIVT 143
QY 114 VSSGGSGSGGGSGGSGSVMTQTPLTISVTIGQPASISCKSSQSLDSDGKTYINMLL 173
DB 144 VSSGGSGSGGGSGGSGSVMTQTPLTISVTIGQPASISCKSSQSLDSDGKTYINMLL 197
QY 174 QRPQSPKRLIYVSKLDSGVDPDRFTGSGSDTFTLKINRVAEDLGVYYCWOGTHTSPIT 233
DB 198 QRPQSPKRLIYVSKLDSGVDPDRFTGSGSDTFTLKINRVAEDLGVYYCWOGTHTSPIT 257
QY 234 FGATKLEIK 243
DB 258 FGATKLEIK 267

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RESULT 6
US-08-661-052-16
/ Sequence 16, Application US/08661052
/ Patent No. 5837243
/ GENERAL INFORMATION:
/ APPLICANT: Yashwant M. Deo
/ APPLICANT: Joel Goldstein
/ APPLICANT: Robert Graziano
/ APPLICANT: Chezia Somasundaram
/ TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISHD
/ TITLE OF INVENTION: OF ANTI-Fc RECEPTOR ANTIBODIES
/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: LAHIVE & COCKFIELD
/ STREET: 60 State Street, Suite 510
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02109-1875
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS

```


FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: MKI-043CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-7414
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-364-088-16

Query Match 69.8%; Score 900; DB 4; Length 553;
Best Local Similarity 68.7%; Pred. No. 1.4e-64;
Matches 171; Conservative 27; Mismatches 35; Indels 16; Gaps 3;

QY 2 VOLQSGAEIVRSAGAVKLSCTASGFNIKDYMHVWKORPEQGLEWIGMIDPENGDTEYA 61
DB 278 IKLQSGAEIVRSAGAVKLSCTASGFNIKDYMHVWKORPEQGLEWIGMIDPENGDTEYA 337
QY 62 PKQKATMTADTSSNTAVILOSLASEDTAVYYCN-----FYDADLDYWGQGTTVY 114
DB 338 PKQKATMTADTSSNTAVILOSLASEDTAVYYCN-----FYDADLDYWGQGTTVY 394
QY 115 SSGGGSGGGSGGGSDVLMQTPLTSLVTTGQPAISCKSSQSLDSDGKTYLWMLQ 174
DB 395 SSGGGSGGGSGGGSENVLTQSPAIMSAPGEKVTITCSASSV-----SYMHWFOQ 448
QY 175 RQSGPKRLIYVSKLDSGVPRFTSGSGDPTLTKINVEARDLVVYCWGQTHPLTF 234
DB 449 KQTSKRLMTYTSNLASGVPARFSSGSGTISLTISRWEADAAVTCQQRSSYPLTF 508
QY 235 GAGTKLEIK 243
DB 509 GAGTKLEIK 517

RESULT 9
US-09-102-716-16
Sequence 16, Application US/09102716
Patent No. 6395272
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
Joel Goldstein
Robert Graziano
Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,716
FILING DATE: 22-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MKI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-102-716-16

Query Match 69.8%; Score 900; DB 4; Length 553;
Best Local Similarity 68.7%; Pred. No. 1.4e-64;
Matches 171; Conservative 27; Mismatches 35; Indels 16; Gaps 3;

QY 2 VOLQSGAEIVRSAGAVKLSCTASGFNIKDYMHVWKORPEQGLEWIGMIDPENGDTEYA 61
DB 278 IKLQSGAEIVRSAGAVKLSCTASGFNIKDYMHVWKORPEQGLEWIGMIDPENGDTEYA 337
QY 62 PKQKATMTADTSSNTAVILOSLASEDTAVYYCN-----FYDADLDYWGQGTTVY 114
DB 338 PKQKATMTADTSSNTAVILOSLASEDTAVYYCN-----FYDADLDYWGQGTTVY 394
QY 115 SSGGGSGGGSGGGSDVLMQTPLTSLVTTGQPAISCKSSQSLDSDGKTYLWMLQ 174
DB 395 SSGGGSGGGSGGGSENVLTQSPAIMSAPGEKVTITCSASSV-----SYMHWFOQ 448
QY 175 RQSGPKRLIYVSKLDSGVPRFTSGSGDPTLTKINVEARDLVVYCWGQTHPLTF 234
DB 449 KQTSKRLMTYTSNLASGVPARFSSGSGTISLTISRWEADAAVTCQQRSSYPLTF 508
QY 235 GAGTKLEIK 243
DB 509 GAGTKLEIK 517

RESULT 10
US-09-646-028-12
Sequence 12, Application US/09646028
Patent No. 6562347
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: 2000-09-12
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 12
LENGTH: 348
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence://note=synthetic construct
US-09-646-028-12

Query Match 67.2%; Score 866; DB 4; Length 348;
Best Local Similarity 65.3%; Pred. No. 4.4e-62;
Matches 160; Conservative 37; Mismatches 46; Indels 2; Gaps 1;

QY 1 VOLQSGAEIVRSAGAVKLSCTASGFNIKDYMHVWKORPEQGLEWIGMIDPENGDTEYA 60
DB 98 EVQLQSGSDPLVKPKMSVYKLSKTLTGYNFSDRRIMWQKPERGLEGWGRIDPSGDDTY 157
QY 61 AKFQKATMTADTSSNTAVILOSLASEDTAVYYCNFYGD--ALDYWGQGTTVYSSGG 118

Fri Aug 6 16:44:40 2004

us-09-297-181-2.ra1

Page 6

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DB 158 NADFKTPATLTVDRPSNTAYLEISNLTSGDSAVYYCSIGDYACDIWGCGTELTIVSSG 217
QY 119 GSGGGGGGGGGGGGSDVMTQTPLTSLVTTIGQPASISCKSSQSLNDSGKTYLWMLQRPQ 178
DB 218 GSGGGGGGGGGGGGSDVMTQTPLTSLVTTIGQPASISCKSSQSLNDSGKTYLWMLQRPQ 277
QY 179 SPKRLIYVSKLDSGVPDRFTSGSGGTDFTLKINRYEADLGYIYCCQGHSPLTGAGT 238
DB 278 SPKRLIYVSKSRFPFVPERFSGSGGTDFTLKISRVEAEDLGYIFCSQGAHVEMTFGGGT 337
QY 239 KLEIK 243
DB 338 KLEVK 342

RESULT 11
US-09-646-028-14
; Sequence 14, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biraqyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FASTSEQ for windows version 3.0
; SEQ ID NO 14
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of artificial sequence: /note=synthetic construct
; US-09-646-028-14

Query Match 67.2%; Score 866; DB 4; Length 361;
Best Local Similarity 65.3%; Pred. No. 4.6e-62;
Matches 160; Conservative 37; Mismatches 46; Indels 2; Gaps 1;

QY 1 QVQLQSGAEIVRSASVSKLSTASGENIKDYMMHWKQRPQGLEWIGMIDPENGTREY 60
DB 111 EVQLQSGPDLVYKPGMSVKLSCKTLGYNFSDKRHHMTKQKRGRLIEWVGRIDPSNGDTDY 170
QY 61 APRKQKATMTADTSSNTAYLQSLASEDTAVYYCNFYD--ALDYWGQGTIVTVSSGG 118
DB 171 NADPKTPTATLVDRPSNTAYLEISNLTSGDSAVYYCSIGDYACDIWGCGTELTIVSSG 230
QY 119 GSGGGGGGGGGGGGSDVMTQTPLTSLVTTIGQPASISCKSSQSLNDSGKTYLWMLQRPQ 178
DB 231 GSGGGGGGGGGGGGSDVMTQTPLTSLVTTIGQPASISCKSSQSLNDSGKTYLWMLQRPQ 290
QY 179 SPKRLIYVSKLDSGVPDRFTSGSGGTDFTLKINRYEADLGYIYCCQGHSPLTGAGT 238
DB 291 SPKRLIYVSKSRFPFVPERFSGSGGTDFTLKISRVEAEDLGYIFCSQGAHVEMTFGGGT 350
QY 239 KLEIK 243
DB 351 KLEVK 355

RESULT 12
US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; APPLICANT: BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
```

```
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pillsbury Winthrop, L.L.P.
;; STREET: 1100 New York Ave., N.W.
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: MS word
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/423,439
;; FILING DATE: 09-NOV-1999
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB98/01294
;; FILING DATE: 05-MAY-1998
;; APPLICATION NUMBER: GB 9709421.3
;; FILING DATE: 10-MAY-1997
;; INFORMATION FOR SEQ ID NO: 38:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 288 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38

Query Match 65.4%; Score 843.5; DB 4; Length 288;
Best Local Similarity 66.3%; Pred. No. 2.3e-60;
Matches 165; Conservative 31; Mismatches 46; Indels 7; Gaps 3;
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QY 1 QVQLQSGAEIVRSASVSKLSTASGENIKDYMMHWKQRPQGLEWIGMIDPENGTREY 60
DB 23 QVQLQSGPDLVYKPGMSVKLSCKTLGYNFSDKRHHMTKQKRGRLIEWVGRIDPSNGDTDY 82
QY 61 APRKQKATMTADTSSNTAYLQSLASEDTAVYYCNFYD--ALDYWGQGTIVTVSSGG 115
DB 83 NEKRNKATLTIVKSSSTTAAWQSLTSEDSAVYYCARERAYGYDDMDYWGQGTIVTVS 142
QY 116 GSGGGGGGGGGGGGSDVMTQTPLTSLVTTIGQPASISCKSSQSLNDSGKTYLWMLQ 174
DB 143 GSGGGGGGGGGGGGSDVMTQTPLTSLVTTIGQPASISCKSSQSLNDSGKTYLWMLQ 202
QY 175 RPQSPKRLIYVSKLDSGVPDRFTSGSGGTDFTLKINRYEADLGYIYCCQGHSP 234
DB 203 RPQSPKRLIYVMASTRFTSGVPDRFTSGSGGTDFTLTISVQAEADLAIYCKQ--SYLR 261
QY 235 GAGTKLEIK 243
DB 262 GGGTKLEIK 270

RESULT 13
US-09-184-658-63
; Sequence 63, Application US/09184658
; Patent No. 6030792
; GENERAL INFORMATION:
; APPLICANT: Olteneas, Ivan G.
; APPLICANT: Mezes, Peter S.
; APPLICANT: Downs, James T.
; APPLICANT: Johnson, Kimberly S.
; TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
; FILE REFERENCE: PC9946-A
; CURRENT APPLICATION NUMBER: US/09/184,658
; EARLIER APPLICATION NUMBER: 60/065,423
; EARLIER FILING DATE: 1997-11-13
; NUMBER OF SEQ ID NOS: 69
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QY 1 QVQLQQSAGELVRSASVYLCTAAGFENIKDYYIMHWKORPEGGFLWIGMDPENDPTTEY 60
Db 23 EVQLVESGGSGSVQPGSLKLSCTAASGFTNTYIGMSWRVOTPPKRLIEWATINSGLTTEY 82
QY 61 APRKQKRAITMDITSSNTAYITQLSLASEDTAVYYCNFYGDALDYWGCGTIVYVSSGGGG 120
Db 83 ADVYKGRITTSRDNAKNTLYIQMNRLLKSGDSIMYVCVRGYSYARWGCGALTVSSSGGGG 142
QY 121 SGGGSGSGGGG-SDVIMLTQTPILTSYTIQGPASISCKSSQSLDSDPKTYINMLIQRPQGS 179
Db 143 SGGGSGSGGGGSDVIMLTQTPILTSYTIQGSNBSICKSSQSLDGSDELTYINMLIQRPQGS 202
QY 180 PKRLIIVYSKLDGVPDRFTSGSGSDTFLTKINRYAEADLGYYICQGHSPITFGAGTK 239
Db 203 PKRLIIVSELDSGVPRFTSGSGSDTFLTKISRAEADLGYYICCGQTHFPHTFGAGTK 262
QY 240 LEIK 243
Db 263 LEIK 266

RESULT 14
US-09-504-262D-63
Sequence 63, Application US/09504262D
Patent No. 6642007
GENERAL INFORMATION:
APPLICANT: Pfizer Inc.
APPLICANT: Saltarelli, Mary J.
APPLICANT: Johnson, Kimberly S.
APPLICANT: O'Brien, Ivan G.
TITLE OF INVENTION: Assays for Measurement of Type II Collagen Fragments in Urine
PIR REFERENCE: P010896GR - CIP of P03946A
CURRENT APPLICATION NUMBER: US/09/504,262D
CURRENT FILING DATE: 2000-02-15

```

QY      1 OVLOOQSGAEIVRSQASVYKLSCTPAGFNIDKDYMHVMVVKQREPGGLWETGWIIDPENGPTEY      60
Db      23 KQIVRSVGGGASVQPPGSLKLSCTASGFTFFNNYGNMSWVRQTPDKRUBWATINSGGLTFY      82
QY      61 AEPFOGAKTMTADTSSNTAVYQLQSSIASBEDTAVVYCNFPGDALPYGQGVTVIVSSG3GG      120
Db      83 ADSVKGREFTISDNKAKNTLYLQMRNLKSGSGMYCVARGYNVARMGGLALVTYSSGGG      142
QY      121 SGGGSGGGGGG-SDVMTQTPILTSTTIOQPSISCKSSQSLISBDGKTYLWMLQRPQGS      179
Db      143 SGGGSGGGGGSDVVMYQTPLTSLVTLGQASISCKSSQSLISGDBGTYLWMLQRPQGS      202
QY      180 PRRLIYVSKLDSGVDPDFRTSGSGSTDTPLKINRVEADLGVVYCMOQTHSPITFGAGTK      235
Db      203 PRRLIFVSELDGVPDRFTSGSGSTDTPLKISRAEADLGVVYCCQSTHPRHFGAGTK      262
QY      240 LEIK      243
Db      263 LEIK      266

RESULT 15
US-09-423-439-32
; Sequence 32, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:

```

ADDRESSER: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-423-439-32

Query Match 65.4%; Score 843.5; DB 4; Length 673;
Best Local Similarity 66.3%; Pred. No. 6e-60;
Matches 165; Conservative 31; Mismatches 46; Indels 7; Gaps 3;

QY 1 QVQLQSGAEIVKSGASVSKLSTAGSEINIKDYMMHWKQRPQGLWIGWIDPENGDTTEY 60
DB 20 QVQLQSGAEIVKSGASVSKLSTAGSEINIKDYMMHWKQRPQGLWIGWIDPENGDTTEY 79
QY 61 APRKQKATMTADTSSNTAYLQLSLASEDTAVYYC-----NFGDALDYWGQGTIVTVS 115
DB 80 NEKFKNATLTVDKSSFTAYWQLSLTSEDSAVYYCARERAYGYDAMDYWGQGTIVTVS 139
QY 116 SGSGSGSGSGSGSGSVLMTQTPLTSLVITIGQSPASISCKSSQSLTDS-DGKTYLAWLLQ 174
DB 140 SGSGSGSGSGSGSGSDIELSQSPSLAVSAGEKVTWVSCSSQSLNSRTRKNLANYQQ 199
QY 175 RFGQSPRLIYLVKSLDSGVDPDRFTSGSGSGDTFTLKINRYAEADLGYYCWCQGTSPDTE 234
DB 200 RFGQSPRLIYLVKSLDSGVDPDRFTSGSGSGDTFTLKINRYAEADLGYYCWCQGTSPDTE 258
QY 235 GAGTKLEIK 243
DB 259 GAGTKLEIK 267

Search completed: July 30, 2004, 11:22:26
Job time : 15.3232 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2004, 11:16:36 ; Search time 13.3354 Seconds
(without alignments)
1752.823 Million cell updates/sec

Title: US-09-297-181-2

Perfect score: 1289

Sequence: 1 QVQLQSGAEIVRSGASVXL.....CWQGTSPILTFAGTLEIK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR_78:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	912.5	70.8	249	2 S41374	single chain Fv an
2	832.5	64.6	233	2 JC5322	p53 specific singl
3	815	63.2	268	2 A56446	Ig heavy chain V r
4	560	43.4	132	2 C32513	Ig kappa chain pre
5	553	42.9	113	2 F30560	Ig kappa chain V r
6	545.5	42.3	136	2 S04576	Ig heavy chain pre
7	541	42.0	112	2 A55491	proteolytic antibo
8	539	41.8	112	2 A36259	Ig kappa chain V r
9	537	41.7	111	2 S20709	Ig kappa chain V r
10	528	41.0	116	2 S15672	Ig heavy chain V r
11	527	40.9	112	2 PL0273	Ig heavy chain V r
12	517	40.1	137	2 S52445	Ig heavy chain V r
13	511	39.6	101	2 A33730	Ig kappa chain V r
14	509.5	39.5	120	2 S03471	Ig heavy chain V-D
15	509	39.5	131	2 S31577	Ig kappa chain - m
16	505.5	39.2	118	2 S25174	Ig heavy chain V r
17	500	38.8	178	2 S29594	Ig gamma chain (WM
18	488	37.9	122	2 S06823	Ig heavy chain V r
19	487.5	37.8	117	2 S17586	Ig heavy chain V r
20	485.5	37.7	120	2 S03482	Ig heavy chain V-D
21	479.5	37.2	221	2 S49220	Ig gamma-1 chain -
22	476	36.9	133	2 S23330	Ig kappa chain pre
23	474	36.9	142	2 S22020	Ig kappa chain V r
24	475.5	36.9	116	2 S24289	Ig gamma chain V r
25	474.5	36.8	115	2 S03482	Ig heavy chain V-D
26	474	36.8	103	2 PH1055	Ig light chain V r
27	473	36.7	133	2 S42611	HUNWK protein prec
28	472	36.6	133	2 S40322	Ig kappa chain V r
29	471	36.5	108	2 PH1012	Ig heavy chain V r

30	469	36.4	91	2 S42186	Ig kappa chain V r
31	469	36.4	133	1 K2HURP	Ig kappa chain pre
32	468.5	36.3	140	2 S22658	Ig kappa chain pre
33	465	36.1	103	2 PH1056	Ig light chain V r
34	464.5	36.0	144	2 B30502	Ig heavy chain V r
35	463	35.9	118	2 S40374	Ig kappa chain - h
36	462	35.8	114	4 A47271	nitrophenyl phosph
37	461	35.8	133	1 A24452	Ig kappa chain pre
38	460.5	35.7	114	2 B49002	Ig kappa chain V r
39	460	35.7	112	2 A31807	Ig kappa chain V r
40	458.5	35.6	114	2 S49572	Ig kappa chain pre
41	453	35.1	122	2 S40338	Ig kappa chain - h
42	451	35.0	131	2 B39276	Ig light chain pre
43	450	34.9	115	2 S38715	Ig kappa chain V r
44	449	34.8	132	2 S40322	Ig kappa chain V r
45	447	34.7	112	2 S38719	Ig light chain V r

ALIGNMENTS

RESULT 1

S41374
single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C/Accession: S41374

R/Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antibody

A/Reference number: S41374

A/Accession: S41374

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-249 <ART>

A/Cross-references: EMBL:229480

Query Match 70.8%; Score 912.5; DB 2; Length 249;
Best Local Similarity 72.5%; Pred. No. 8.2e-59;

Matches 179; Conservative 25; Mismatches 38; Indels 5; Gaps 2;

QY	1	QVQLQSGAEIVRSGASVXLCTASGFNIDYMMHWVKRPEQGLTWIGMDENGDT	60
DB	1	QVQLQSGAEIVRSGASVXLCTASGFNIDYMMHWVKRPEQGLTWIRIAPASGVK	60
QY	61	APKFGKATMTDTSNTYLLQSLASGDTAVYTC---NFGDALDIWGGSTVTVSS	116
DB	61	VERFQDKATITADTSNTAYLLSLTSDITAVYYCARRDITY-TSLGWGQGSTVTVSS	119
QY	117	GGGSGGGSGGGSDVMTQTPLTSTVITIGDPASTSCSSQSLSDSGTVMNLLORP	176
DB	120	RGGSGGGSGGGSDIETQSPPVVYTPGSVSTSCSSSKSLTSDSGSYTFWLLQRP	179
QY	177	GQSPKRLIYLVKLDGVPDRFTGSGSGDTFTLKINRVAEDLVGVVYCWQGTSP	236
DB	180	GQSPQLIRFMNSLNSGVDRFSGSGSGSFTLRLSRVAEDLVGVVYCWQHETPL	239
QY	237	GTKLK 243	
DB	240	GTKLK 246	

RESULT 2
p53 specific single-chain antibody Pab421 - human
C/Species: Homo sapiens (man)
C/Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C/Accession: JC5322
R/Jannet, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A/Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A/Reference number: JC5322; MUID:97168950; PMID:9016757
A/Accession: JC5322

A:Molecule type: mRNA
 A:Residues: 1-233 <JAN>
 A:Experimental source: hydriocoma cell
 C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 64.6%; Score 832.5; DB 2; Length 233;
 Best Local Similarity 68.9%; Pred. No. 4,4e-53;
 Matches 164; Conservative 25; Mismatches 44; Indels 5; Gaps 3;

QY 5 QQSAGELVRSAGSVKLSCTASGFNIKDYMHVWKORPEQGLEWIGWIDPENGDTEYAPKR 64
 DB 1 QESGAEIVRSAGSVKLSCTTSGFNINDYMHVWKORPEQGLEWIGRIDPENGDADMRSS 60

QY 65 QGKATMTADTSSNTAYQLSSLASSEDYAVYCNFYGDALDYWGQCTTVTVSSGGSGSGG 124
 DB 61 GVKATMTADTSSNTAYQLSSLTSEDYAVYCN--AGMDYWGQCTTVTVSSGGSGSGGR 117

QY 125 GSGGGSDVMTQCPPLTSLTIGQPASISCKSSQSLDSDGKTYLNMILQRPQSPKRLT 184
 DB 118 ASGGGSDILTQSPALAVSLGRATISCRASKS-VSTGYSYMHVWQKRPQGPRLLI 176

QY 185 YIVSKLDSGVDPDRFTSGSGTDFTLKINRYEADLGYVYCWQTHSPLTGAGTKLEI 242
 DB 177 YIVSNLESQVPARRSSGSGTDFTLNHPVREEDAAITYC-QHIRELTRESGTKLEI 233

RESULT 3

A56446
 Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)
 C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C/Accession: A56446
 C/Tang, P.M.; Mahoney, W.C.; Folitz, L.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity diognin-binding protein displayed on M13 is functionally ident

A:Reference number: A56446; MUID:9522583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-268 <TRAN>

A:Cross-references: GB:U20617

C:Keywords: heterotetramer; immunoglobulin

Query Match 63.2%; Score 815; DB 2; Length 268;
 Best Local Similarity 64.5%; Pred. No. 9.4e-52;
 Matches 158; Conservative 30; Mismatches 49; Indels 8; Gaps 3;

QY 1 QVOIQSGAEIVRSAGSVKLSCTASGFNIKDYMHVWKORPEQGLEWIGWIDPENGDTEY 60
 DB 3 QVKIQSGAEIVRSAGSVKLSCTTSGFNINDYMHVWKORPEQGLEWIGRIAPANGITKY 62

QY 61 APEQKATMTADTSSNTAYQLSSLASSEDYAVYCNFYGDALD-YWGQCTTVTVSSGG 118
 DB 63 DPKQKATMTADTSSNTAYQLSSLTSEDYAVYCNFYGDALD-YRYENWQCTTVTVSSGG 122

QY 119 GSGGGSGSGSDVMTQCPPLTSLTIGQPASISCKSSQSLDSDGKTYLNMILQRPQ 178
 DB 123 GSGGGSGSGSDILTQSPALAVSLGRATISCRASKS-VSTGYSYMHVWQKRPQGPRLLI 176

QY 179 SPKRLIYVSKLDSGVDPDRFTSGSGTDFTLKINRYEADLGYVYCWQTHSPLTGAGT 238
 DB 177 SPKLMVYVTSHPVAPARFSGSGSGNSYSLTSSMEQEDAAITYCQGFPSPTFGSGT 236

QY 239 KLEIK 243
 DB 237 KLEIK 241

RESULT 4
 C32513
 Ig kappa chain precursor V region (BXW14) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C/Accession: C32513

R/Kotler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;

J. Clin. Invest. 82, 852-860, 1988

A:Title: Immunoglobulin kappa 194t chain variable region gene complex organization and

A:Reference number: A94689; MUID:8831394; PMID:3138286

A/Accession: C32513

A:Molecule type: DNA

A:Residues: 1-132 <KOF>

A:Cross-references: GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:g196940

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F/36-115/Domain: immunoglobulin homology <IM>

Query Match 43.4%; Score 560; DB 2; Length 132;
 Best Local Similarity 95.5%; Pred. No. 1e-33;
 Matches 107; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 132 DVMTQCPPLTSLTIGQPASISCKSSQSLDSDGKTYLNMILQRPQSPKRLIYVSKLD 191
 DB 21 DVMTQCPPLTSLTIGQPASISCKSSQSLDSDGKTYLNMILQRPQSPKRLIYVSKLD 80

QY 192 SGVPDRFTSGSGTDFTLKINRYEADLGYVYCWQTHSPLTGAGTKLEI 243
 DB 81 SGVPDRFTSGSGTDFTLKISRVAEDLGYVYCWQTHSPRTGGTKLEIK 132

RESULT 5

F30560
 Ig kappa chain V region (28.4.10A) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C>Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000

C/Accession: F30560

R/Matsuda, T.; Kabat, E.A.

J. Immunol. 142, 863-870, 1989

A:Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclon

A:Reference number: A30560; MUID:89110062; PMID:2464028

A/Accession: F30560

A/Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <MAT>

A:Cross-references: GB:M24273; NID:g197081; PIDN:AAA63370.1; PID:g197082

C:Superfamily: Immunoglobulin V region; Immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F/16-95/Domain: immunoglobulin homology <IM>

Query Match 42.9%; Score 553; DB 2; Length 113;
 Best Local Similarity 94.6%; Pred. No. 2.8e-33;
 Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 132 DVMTQCPPLTSLTIGQPASISCKSSQSLDSDGKTYLNMILQRPQSPKRLIYVSKLD 191
 DB 1 DVMTQCPPLTSLTIGQPASISCKSSQSLDSDGKTYLNMILQRPQSPKRLIYVSKLD 60

QY 192 SGVPDRFTSGSGTDFTLKINRYEADLGYVYCWQTHSPLTGAGTKLEI 243
 DB 61 SGVPDRFTSGSGTDFTLKISRVAEDLGYVYCWQTHSPRTGGTKLEIK 112

RESULT 6
 S04576
 Ig heavy chain precursor V region (MR1-histone 7H) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 42.3%; Score 545.5; DB 2; Length 136;
Best Local Similarity 88.9%; Pred. No. 1.2e-32;
Matches 104; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 1 QVQLQSGAEIVSGASVKLSCTASGFINIKDYHWKQKPEQGLEWIGIDPENGTLEY 60
Db 20 EVQLQQSGAEIVSGASVKLSCTASGFINIKDYHWKQKPEQGLEWIGIDPENGTLEY 79
QY 61 APFQKATMTADTSSNTAVIQLSLASEPTAVYVCFYGD-ALDYGGCTTAVSS 116
Db 80 ASFQKATMTADTSSNTAVIQLSLASEPTAVYVCFYGTGAVADYWGQGSIVTVSS 136

RESULT 7

A55491
proteolytic antibody light chain - mouse

C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 21-Jan-2000
C;Accession: A55491
R;Geo, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.; Massey, R.
J. Biol. Chem. 269, 32389-32393, 1994
A;Title: Molecular cloning of a proteolytic antibody light chain.
A;Reference number: A55491; MUID:95096089; PMID:7798238
A;Accession: A55491
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <GAP>

A;Cross-references: GB:L34775
A;Note: authors translated the codon TAT for residue 37 as Thr
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 42.0%; Score 541; DB 2; Length 112;
Best Local Similarity 92.9%; Pred. No. 2e-32;
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 132 DVIMTQPLTLSTVITIGQPASISCKSSQSLSDGKTYLWMLQRPQSPKRLIYVSKLD 191
Db 1 DVIMTQPLTLSTVITIGQPASISCKSSQSLSDGKTYLWMLQRPQSPKRLIYVSKLD 60
QY 192 SGVPDRFTSGSGTDFTLKINRYEADLVGYVCMQGHSPITFGAGTKLEIK 243
Db 61 SGVPDRFTSGSGTDFTLKINRYEADLVGYVCMQGHSPITFGAGTKLEIK 112

RESULT 8

A36259
Ig kappa chain V region (TR34) - mouse

C;Species: Mus musculus (house mouse)
C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 21-Jan-2000
C;Accession: A36259
R;Allber, B.; Scherf, T.; Levitt, M.; Anglister, J.
Biochemistry 29, 10032-10041, 1990
A;Title: NMR-derived model for a peptide-antibody complex.
A;Reference number: A36259; MUID:91104915; PMID:2271636
A;Accession: A36259
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <ZILL>
A;Cross-references: GB:M30458; GB:M30459; GB:M30460; GB:M30481; GB:M30482; GB:M30483
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 41.8%; Score 539; DB 2; Length 112;
Best Local Similarity 92.9%; Pred. No. 2.8e-32;
Matches 104; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 132 DVIMTQPLTLSTVITIGQPASISCKSSQSLSDGKTYLWMLQRPQSPKRLIYVSKLD 191
Db 1 DVIMTQPLTLSTVITIGQPASISCKSSQSLSDGKTYLWMLQRPQSPKRLIYVSKLD 60
QY 192 SGVPDRFTSGSGTDFTLKINRYEADLVGYVCMQGHSPITFGAGTKLEIK 243
Db 61 SGVPDRFTSGSGTDFTLKINRYEADLVGYVCMQGHSPITFGAGTKLEIK 112

RESULT 9

S20709
Ig kappa chain V region - mouse

C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S20709
R;Brenand, D.M.; Hands, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; O
submitted to the EMBL Data Library, April 1992
A;Description: Binding specificity and variable region sequences of two monoclonal ant
A;Reference number: S20706
A;Accession: S20709
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-111 <SRE>
A;Cross-references: EMBL:Z11917; NID:952655; PIDN:CAA77975.1; PID:952656
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 41.7%; Score 537; DB 2; Length 111;
Best Local Similarity 91.9%; Pred. No. 3.9e-32;
Matches 102; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 132 DVIMTQPLTLSTVITIGQPASISCKSSQSLSDGKTYLWMLQRPQSPKRLIYVSKLD 191
Db 1 DVIMTQPLTLSTVITIGQPASISCKSSQSLSDGKTYLWMLQRPQSPKRLIYVSKLD 60
QY 192 SGVPDRFTSGSGTDFTLKINRYEADLVGYVCMQGHSPITFGAGTKLEIK 242
Db 61 SGVPDRFTSGSGTDFTLKINRYEADLVGYVCMQGHSPITFGAGTKLEIK 111

RESULT 10

S15672
Ig heavy chain V region - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S15672
R;Tempest, P.R.; Brenner, P.; Lambert, M.; Taylor, G.; Furze, J.M.; Carr, F.J.; Harris
Bio/Technology 9, 266-271, 1991
A;Title: Reshaping a human monoclonal antibody to inhibit human respiratory syncytial
A;Reference number: S15672; MUID:91337412; PMID:1367535
A;Accession: S15672
A;Status: Preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-116 <TEM>
A;Cross-references: EMBL:X58835; NID:951978; PIDN:CAA41644.1; PID:951979
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 41.0%; Score 528; DB 2; Length 116;
Best Local Similarity 84.3%; Pred. No. 1.8e-31;
Matches 97; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 2 VOLQSGAEIVSGASVKLSCTASGFINIKDYHWKQKPEQGLEWIGIDPENGTLEYA 61
Db 2 VOLQSGAEIVSGASVKLSCTASGFINIKDYHWKQKPEQGLEWIGIDPENGTLEYA 61
QY 62 PKFQKATMTADTSSNTAVIQLSLASEPTAVYVCFYGDALDYWGQCTTAVSS 116
Db 62 PKFQKATMTADTSSNTAVIQLSLASEPTAVYVCFYGDALDYWGQCTTAVSS 116

\$31577

Ig kappa chain - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence revisited

C:/date: 20-Feb-1995 #sequence_ revision 20-Feb-1995 #text_change 21-Jan-2000
C:/Accession: 531577

R;Recinos, A.; Silv

submitted to the EMBL Data Library, January 1993

A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for two anti

A/Reference number: S31577
A/Accession: S31577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-131 <REF

A; Cross-references: EMB
C; Superfamily: immunoglob

C;Keywords: heterotetrahedron; immunoglobulin; superfamily; C;Keywords: heterotetrahedron

F;35-114/Domain: immunoglobulin homology <IMM>

Answer: Match

Query Match	39.5%	Score	509;
Best Local Similarity	86.6%	Pred	No

Best Local Similarity 86.6%; Pred. No. 4.8e-30;
Matches 97; Conservative 6; Mismatches 9. Indels

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sequence 21 conservative 0; mismatches 9; indels 0; gaps 0;

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QY 132 DVLMQTPLTSTIGOPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLIYLVSKLD 191

[illegible]

192 SGVPDREFTGSGSTDEFTI KINRYEAENDI CIVVVCWOCMECHDI MEQAQCEATITR 343

192 SGVPDRITGSSGIDFTLKINRVEAEDLGVIYCMQGTHSPLTFGAGTKLEIK 243

Db 80 SGVPDFSGSGSDFTLRISRVEADLDGVYYCMONTHPPYTFGGCKLEMK 131

13

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Search completed: July 30, 2004, 11:21:46
Job time : 14.3354 secs
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Job time : 14.3354 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 30, 2004, 11:15:41 ; Search time 7.90244 Seconds
(without alignments)
1601.157 Million cell updates/sec

Title: US-09-297-181-2
Perfect score: 1289
Sequence: 1 QVQLQSGAEIVRSASVKL.....CWOGTHSPITFGATKLEIK 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query	Match Length	ID	Description
1	469	36.4	133	1	P06310 homo sapien
2	428	33.2	113	1	P01615 homo sapien
3	428	33.2	113	1	P01617 homo sapien
4	428	33.2	113	1	P01631 mus musculu
5	423	32.8	117	1	P06309 homo sapien
6	423	32.8	139	1	P01751 mus musculu
7	418.5	32.5	115	1	P01614 homo sapien
8	405.5	31.5	120	1	P01747 mus musculu
9	399	31.0	137	1	P01755 mus musculu
10	397.5	30.8	140	1	P01746 mus musculu
11	396.5	30.8	112	1	P01616 homo sapien
12	384.5	29.8	117	1	P01756 mus musculu
13	384	29.8	147	1	P01744 homo sapien
14	382	29.6	113	1	P01628 mus musculu
15	382	29.6	113	1	P01630 mus musculu
16	380.5	29.5	117	1	P01757 mus musculu
17	380	29.3	118	1	P06330 mus musculu
18	378	29.3	112	1	P01626 mus musculu
19	377	29.2	113	1	P03976 mus musculu
20	377	29.2	120	1	P06329 mus musculu
21	375.5	29.1	138	1	P03980 mus musculu
22	372.5	28.9	111	1	P01666 mus musculu
23	372.5	28.9	136	1	P01759 mus musculu
24	371	28.8	112	1	P01625 mus musculu
25	367.5	28.5	111	1	P01665 mus musculu
26	367.5	28.5	121	1	P01745 mus musculu
27	365.5	28.4	108	1	P01618 canis fami
28	365.5	28.4	111	1	P01667 mus musculu
29	364	28.2	117	1	P01753 mus musculu
30	363.5	28.2	111	1	P01664 mus musculu
31	360.5	28.0	111	1	P01668 mus musculu
32	359	27.9	110	1	P01669 mus musculu
33	358.5	27.8	134	1	P06314 homo sapien

34	358	27.8	117	1	P01750 mus musculu
35	352	27.3	117	1	P01748 mus musculu
36	352	27.3	117	1	P06328 mus musculu
37	351	27.2	117	1	P01743 homo sapien
38	350.5	27.2	111	1	P01673 mus musculu
39	350.5	27.2	114	1	P01625 homo sapien
40	349.5	27.1	111	1	P01673 mus musculu
41	348.5	27.0	111	1	P01671 mus musculu
42	348	27.0	117	1	P01754 mus musculu
43	348	27.0	117	1	P06327 mus musculu
44	347.5	27.0	111	1	P01660 mus musculu
45	345.5	26.8	131	1	P01661 mus musculu

ALIGNMENTS

```

RESULT 1
KV2F_HUMAN          STANDARD;          PRT;          133 AA.
ID   P06310;
AC   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ig kappa chain V-II region RPMI 6410 precursor.
OS   Homo sapiens (Human) .
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NC   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86041852; PubMed=2997711;
RA   Klobbeck H G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT   "Human immunoglobulin kappa light chain genes of subgroups II and
RT   III."
RL   Nucleic Acids Res. 13:6499-6513(1985).
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CC   or send an email to license@sib-sib.ch).
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DR   EMBL; Z000020; CAAT7315.1; -.
DR   PIR; A01890; K2HURP.
DR   HSSP; P80362; IMTL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; P:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig_1.
DR   SMART; SM00406; IGV_1.
DR   PROSITE; PS00835; IG_LIKE; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL          1..20
FT   CHAIN           21..133
FT   DOMAIN          21..43
FT   DOMAIN          44..59
FT   DOMAIN          60..74
FT   DOMAIN          75..81
FT   DOMAIN          82..113
FT   DOMAIN          114..122
FT   DOMAIN          123..132
FT   DISULFID        43
FT   NON_TER         133
SQ   SEQUENCE       133 AA; 14707 MW; 513CCACAP3673009EE CRC64;
Query Match          36.4%; Score 469; DB 1; Length 133;
Best Local Similarity 76.7%; Pred. No. 1e-29;
Matches 89; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

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RN [1]
RC SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
RU Biochemistry 22:1153-1158(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
CC PROTEIN THAT BINDS DIGOXIN.
DR PIR; A01914; KXMS26.
DR HSSP; P80362; 1MTL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 FRAMEWORK-2.
FT DOMAIN 40 54 FRAMEWORK-3.
FT DOMAIN 55 61 FRAMEWORK-4.
FT DOMAIN 62 93 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 103 112 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 123 93 FRAMEWORK-4.
FT NON_TER 113 113 BY SIMILARITY.
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match
Best Local Similarity 33.2%; Score 428; DB 1; Length 113;
Matches 83; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 132 DVLMQTPTLTSTVIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSPKRLIYVSKLD 191
DB 1 DVVMQTPTLSLVSIGDQASISCRSSQSLVHSGNNTYLMWYIQKAGQSPKRLIYKSNRF 60

QY 192 SCVDPFRFGSGSGGDTFTLKINRVEADLVGYVCWGQTHSPLTFGAGTKLEIK 243
DB 61 SCVDPFRFGSGSGGDTFTLKISRVEADLVGYVCWGQTHSPLTFGAGTKLEIK 112

RESULT 5
KVZE_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DC 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RU diversity.";
RU Nature 309:73-76(1984).
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CC
CC EMBL; 200009; -; NOT_ANNOTATED_CDS.
CC PIR; A01889; K2HUGM.
CC HSSP; P80362; 1MTL.

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DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; F:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL 1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 5 27 FRAMEWORK-1.
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 58 FRAMEWORK-2.
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 66 97 FRAMEWORK-3.
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 107 116 FRAMEWORK-4.
FT DISULFID 127 97 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719B558B1 CRC64;

Query Match
Best Local Similarity 32.8%; Score 423; DB 1; Length 117;
Matches 81; Conservative 15; Mismatches 20; Indels 0; Gaps 0;

QY 128 GGGSDVLMQTPTLTSTVIGQPASISCKSSQSLDSDGKTYLNMLLQRPQSPKRLIYV 187
DB 1 GGGSDVLMQTPTLTSTVIGQPASISCKSSQSLVHSGNNTYLMWYIQKAGQSPKRLIYK 60

QY 188 SKLDGVPDRFRFGSGSGGDTFTLKINRVEADLVGYVCWGQTHSPLTFGAGTKLEIK 243
DB 61 SNRAGVDPFRFGSGSGGDTFTLKISRVEADLVGYVCWGQTHSPLTFGAGTKLEIK 116

RESULT 6
HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE IG heavy chain V region Bl-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paekind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RU Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE Bl-8 MU CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC
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CC
CC EMBL; J00529; AAA8170.1; -.
CC PIR; A90809; MEMS18.
CC PDB; 1A6U; 27-MAY-98.
CC PDB; 1A6W; 15-JUL-98.

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DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DOMAIN 118 124 D SEGMENT.
 FT DOMAIN 125 139 JH2 SEGMENT.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 139 139
 SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;
 Query Match 32.8%; Score 423; DB 1; Length 139;
 Best Local Similarity 67.5%; Pred. No. 3.9e-26;
 Matches 81; Conservative 15; Mismatches 20; Indels 4; Gaps 2;
 QY 1 QVQLQSGAEIVRSGASVYKLSCTASGPNIKDYIMHWKQRPPEGGLMIGWIDENGDTX 60
 DB 20 QVQLQSGAEIVRSGASVYKLSCTASGPNIKDYIMHWKQRPPEGGLMIGWIDENGDTX 79
 QY 61 APFQGAATMTADTSSNTAYLTSLASEDTAVYCC--NFYGA-LDYWGQGTIVYSS 116
 DB 80 NEKFKSKATLTVDKPSSTAYMQSLTSEDAVYICARVYIGSSYVDYWGQGTITLVSS 139
 RESULT 7
 KVZA HUMAN STANDARD; PRT; 115 AA.
 AC P01614;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region Cum.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 OX [1]
 RN RP
 RP SEQUENCE.
 RP MEDLINE=68242259; PubMed=5586923;
 RA Hilschmann N.;
 RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
 RN RP
 RP REVISIONS TO 50: 52; 96 AND 97.
 RP MEDLINE=70063440; PubMed=4188189;
 RA Hilschmann N.;
 RT "Molecular basis of antibody formation.";
 RT Naturwissenschaften 56:195-205(1969).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 CC PIR; B91639; K2HUCM.
 DR HSSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 24 95 BY SIMILARITY.
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12676 MW; 59E9F0A379569EC CRC64;

Query Match 32.5%; Score 418.5; DB 1; Length 115;
 Best Local Similarity 72.6%; Pred. No. 7e-26; Indels 1; Gaps 1;
 Matches 82; Conservative 13; Mismatches 17;
 QY 132 DVLMQTPLTSLVTIGQPASISCKSSQSLDS-DKTYLNLMLQRPQSPKRLIYVSKL 190
 DB 2 DIVMGTPLSLPVTIGEPASISCKSSQSLDSGDGNTYLNWYIQKAGQSPQILYITLSYR 61
 QY 191 DSGVDRFTSGSSGDTFTIKINVEADIGVYCCWQHTSPILFGAGTLEIK 243
 DB 62 ASGVDRFSGSSGDTFTIKISRYVAEDVGYVCMQRIEIPYFGQIKLEIR 114
 RESULT 8
 HV03 MOUSE STANDARD; PRT; 120 AA.
 ID HV03 MOUSE
 AC P01747;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region 36-65.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 OX [1]
 RN RP
 RP SEQUENCE FROM N.A.
 RP MEDLINE=8311846; PubMed=6186498;
 RA Stekevitz M., Gelfer M.L., Brodeur P., Rblert R.,
 RA Marshak-Rothstein A.;
 RT "The genetic basis of antibody production: the dominant anti-arsenate idiotype response of the strain A mouse.";
 RL Eur. J. Immunol. 12:1023-1032(1982).
 CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT. JH2.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Immunoglobulin V region; Hybridoma.
 FT DOMAIN 1 111
 FT NON TER 120 120 Ig-like.
 SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;
 Query Match 31.5%; Score 405.5; DB 1; Length 120;
 Best Local Similarity 65.0%; Pred. No. 7.4e-25;
 Matches 78; Conservative 18; Mismatches 19; Indels 5; Gaps 2;
 QY 2 VOLQSGAEIVRSGASVYKLSCTASGPNIKDYIMHWKQRPPEGGLMIGWIDENGDTX 61
 DB 1 VOLQSGAEIVRSGASVYKLSCTASGPNIKDYIMHWKQRPPEGGLMIGWIDENGDTX 60
 QY 62 PKFGKATMTADTSSNTAYLTSLASEDTAVYCC--NFYGA-LDYWGQGTIVYSS 116
 DB 61 EKFGKATLTVDKPSSTAYMQSLTSEDAVYICARVYIGSSYVDYWGQGTITLVSS 120
 RESULT 9
 HV11 MOUSE STANDARD; PRT; 137 AA.
 ID HV11 MOUSE
 AC P01755;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region S43 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RB Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN GENA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL; J00539; AAA8172.1; -.
DR PIR; A02038; GZMS43.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; AD5881BF44B8E09 CRC64;

Query Match 31.0%; Score 399; DB 1; Length 137;
Best Local Similarity 66.1%; Pred. No. 2.7e-24;
Matches 78; Conservative 10; Mismatches 28; Indels 2; Gaps 1;

QY 1 OVQLOQSGALVYSGASVLSCTASGPNIKDYIMHWKORPQGLEWIGWIDPENGDTXY 60
DB 20 OVQLOQSGALVYSGASVLSCTASGPNIKDYIMHWKORPQGLEWIGWIDPENGDTXY 79
QY 61 APEFGKATMTADTSNTAYLQLSLASEDTAYYCNFY--GPAIDYWGCGTIVTYS 116
DB 80 NEHFKKATLTIDKPESTAYMQLSLTSEDSAVYICARIRLGRFYDWGQGTTLVSS 137

RESULT 10
ID HV02 MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
MEDLINE=82152818; PubMed=6801765;

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RA Sims J., Rabbits T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL; J00493; AAA8128.1; -.
DR PIR; A94264; HWMSG7.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KM Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 30.8%; Score 397.5; DB 1; Length 140;
Best Local Similarity 62.8%; Pred. No. 3.7e-24;
Matches 76; Conservative 19; Mismatches 21; Indels 5; Gaps 2;

QY 1 OVQLOQSGALVYSGASVLSCTASGPNIKDYIMHWKORPQGLEWIGWIDPENGDTXY 60
DB 20 OVQLOQSGALVYSGASVLSCTASGPNIKDYIMHWKORPQGLEWIGWIDPENGDTXY 79
QY 61 APEFGKATMTADTSNTAYLQLSLASEDTAYYCNFY--NFYSDA--LDYWGCGTIVTYS 115
DB 80 NEHFKKATLTIDKPESTAYMQLSLTSEDSAVYICARIRLGRFYDWGQGTTLVSS 139
QY 116 S 116
DB 140 S 140

RESULT 11
ID KV2C HUMAN STANDARD; PRT; 112 AA.
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: This is a Bence-Jones protein.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR007110; Ig_1like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 39 53 FRAMEWORK-2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 92 FRAMEWORK-3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 102 111 FRAMEWORK-4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12055 MW; E5B2E2FA7ABE481 CRC64;
 Query Match 30.8%; Score 396.5; DB 1; Length 112;
 Best Local Similarity 63.4%; Pred. No. 3.4e-24;
 Matches 71; Conservative 25; Mismatches 15; Indels 1; Gaps 1;
 QY 132 DVMTQTEPLTSLVITIGQPASISCKSSQSLSDSGKTYLNLORPGSPKRLTYVSKLD 191
 DB 1 DIVLTQSPSLPYTPGPASISCKSSQNLISBGB-YLDWYTLKPGGSPZLLIITLSNRA 59
 QY 192 SGVEDRFTSGSGGTDFTLKINRYEADIGVYVCWQTHSPLTFGAGTKLEIK 243
 DB 60 SGVFNRRSSGSGGTBFLTKISRVZAEVGYVVCWQALQTLTFCGTNVEIK 111
 RESULT 12
 ID HV12 MOUSE STANDARD; PRT; 117 AA.
 AC P01756;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MOPC 104E.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
 RX MEDLINE=81075344; PubMed=6816276;
 RA Kehry M.R., Fuhman J.S., Schilling J.W., Rogers J., Sibley C.H.,
 RA Hood L.E.,
 RT "Complete amino acid sequence of a mouse mu chain: homology among
 RT heavy chain constant region domains.";
 RL Biochemistry 21:5415-5424(1982).
 CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
 CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC PIR; A02039; MHMS4E.
 DR HSSP; P01789; IMCP.
 DR InterPro; IPR007110; IG_LIKE.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00486; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Glycoprotein.
 FT DOMAIN 1 116 IG_LIKE.
 FT DISULFID 22 96 BY SIMILARITY.
 FT CARBOHD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACB4BE447E41 CRC64;
 Query Match 29.8%; Score 384.5; DB 1; Length 117;
 Best Local Similarity 65.0%; Pred. No. 3e-23;
 Matches 76; Conservative 12; Mismatches 28; Indels 1; Gaps 1;
 QY 1 OVULOQSGAEIVRSAGSYKSLCTAGFENIKDYMMWVYKORPEQGLFWIGIDPENGDTEY 60
 DB 1 EVOULOQSGAEIVRSAGSYKSLCTAGFENIKDYMMWVYKORPEQGLFWIGIDPENGDTEY 60
 QY 61 AEPFGKATMTADTSSNTAYVQLSSLASDFAVYVC-NFYGDALDYWGQTTVTYVSS 116

DB 61 NQFKKOKATLTVDKSSSTAYMQLNLSLSDSAVYVCARDYDWYFDWAGATTVTYVSS 117
 RESULT 13
 ID HV1C HUMAN STANDARD; PRT; 147 AA.
 AC P01744;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V-I region ND precursor (Fragments).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83065234; PubMed=6815656;
 RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
 RA Bell L.O., Gould H.J.;
 RT "Cloning and sequence determination of the gene for the human
 RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
 RN [2]
 RP SEQUENCE OF 20-147.
 RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
 RL (In) Bach M.K. (eds.);
 RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
 RL Marcel Dekker, New York (1978).
 CC -1- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 CC HSSP; P01789; IMCP.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; IG_LIKE.
 DR InterPro; IPR003596; IG_V.
 DR SMART; SM00406; IGV; 1.
 DR Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
 KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 19
 FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
 FT DOMAIN 20 131 IG_LIKE.
 FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 41 115 T->V (IN REF. 2).
 FT CONFLICT 21 21 IH->HI (IN REF. 2).
 FT CONFLICT 53 54 VG->GV (IN REF. 2).
 FT CONFLICT 67 68 MISSING (IN REF. 2).
 FT CONFLICT 125 125
 FT NON_TER 147 147
 SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A536C20 CRC64;
 Query Match 29.8%; Score 384; DB 1; Length 147;
 Best Local Similarity 56.2%; Pred. No. 4.3e-23;
 Matches 72; Conservative 18; Mismatches 26; Indels 12; Gaps 2;
 QY 1 OVULOQSGAEIVRSAGSYKSLCTAGFENIKDYMMWVYKORPEQGLFWIGIDPENGDTEY 60
 DB 20 QTOULOQSGAEIVRSAGSYKSLCTAGFENIKDYMMWVYKORPEQGLFWIGIDPENGDTEY 79
 QY 61 AEPFGKATMTADTSSNTAYVQLSSLASDFAVYVC-NFYGDALDYWGQTTVTYVSS 108
 DB 80 APRFGKATMTADTSSNTAYVQLSSLASDFAVYVC-NFYGDALDYWGQTTVTYVSS 139
 QY 109 GTTIVTSS 116
 DB 140 GTTIVTSS 147
 RESULT 14
 KV2C_MOUSE

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ID      KV2C MOUSE      STANDARD;      PRT;      113 AA.
AC      P01628;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-II region MOPC 511.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=81052016; PubMed=6776396;
RA      Appella E.;
RT      Amino acid sequence of the light chain variable region of M511, a
RL      Mol. Immunol. 17:711-718 (1980).
CC      -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC      BINDS PHOSPHORYLCHOLINE.
DR      PIR; A01910; KWS51.
DR      HSSP; P80362; IWTU.
DR      InterPro; IPR007110; Ig_1Ike.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; Ig; 1.
DR      PROSITE; PS50835; Ig_LIKE; 1.
KW      Immunoglobulin V region.
FT      DOMAIN 1 23 FRAMEWORK-1.
FT      DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT      DOMAIN 40 54 FRAMEWORK-2.
FT      DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT      DOMAIN 62 93 FRAMEWORK-3.
FT      DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT      DOMAIN 103 112 FRAMEWORK-4.
FT      DISULFID 23 93 BY SIMILARITY.
FT      NON TER 113 113
SQ      SEQUENCE 113 AA; 12496 MW; EFBDQ4DA2BD3450 CRC64;

Query Match 29.6%; Score 382; DB 1; Length 113;
Best Local Similarity 67.0%; Pred. No. 4.5e-23;
Matches 75; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY      132 DIVMTQTPILTSTIGQPASISCKSSQSLDSDGKTYINWLLQRPQSPKRLIYVSKD 191
DB      1 DIVITQDELSTKPYTSGSEVSISCRSSKSLIYKDGKTYINWFLQGPQSPRLIYIMSTRA 60

QY      192 SGVPPRFSGSGGTFTLKINRVEADLVGYCCMGCTHSPLPFGAGTKLEIK 243
DB      61 SGVSRFRSGSGGTFTLTISRKADVGVYCCQQLVEYPLTFGAGTKLEIK 112

RESULT 15
KV2F MOUSE
ID      KV2F MOUSE      STANDARD;      PRT;      113 AA.
AC      P01630;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-II region 7S34.1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=83256427; PubMed=6409088;
RA      Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT      "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT      light chains from a mouse hybridoma-derived anti-(streptococcal group
RT      A polysaccharide) antibody containing an additional cysteine residue.
RT      Application of the dimethylaminoazobenzene isothiocyanate technique
RT      for the isolation of peptides.";
RL      Biochem. J. 211:173-180 (1983).

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CC      -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC      ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR      PIR; A01913; KWS575.
DR      HSSP; P80362; IWTU.
DR      InterPro; IPR007110; Ig_1Ike.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; Ig; 1.
DR      PROSITE; PS50835; Ig_LIKE; 1.
KW      Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT      DOMAIN 1 23 FRAMEWORK-1.
FT      DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT      DOMAIN 40 54 FRAMEWORK-2.
FT      DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT      DOMAIN 62 93 FRAMEWORK-3.
FT      DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT      DOMAIN 103 112 FRAMEWORK-4.
FT      DISULFID 23 93 BY SIMILARITY.
FT      NON TER 113 113
SQ      SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 29.6%; Score 382; DB 1; Length 113;
Best Local Similarity 67.0%; Pred. No. 4.5e-23;
Matches 75; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY      132 DIVMTQTPILTSTIGQPASISCKSSQSLDSDGKTYINWLLQRPQSPKRLIYVSKD 191
DB      1 DIVITQDAPSLVTPESVSISCRSSKSLHSNGNTLYLWFLQRPQSCQQLIYRMSNLA 60

QY      192 SGVPPRFSGSGGTFTLKINRVEADLVGYCCMGCTHSPLPFGAGTKLEIK 243
DB      61 SGVPPRFSGSGGTFTLTISRKADVGVYCCQQRREYPLTFGGATKLEIK 112

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Search completed: July 30, 2004, 11:19:46
Job time : 7.90244 secs

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Oy		181	KRLIVLVSFKDLSGVDPRDTGGSGGDFLTKINRVAEDLIQVYWCQTHSPLTGATKL	240
Dd		176	RLLISGATSLETGTGPSRRSSGSGKDYTLSTISQTDEDAVAYYC-QQYWIRTRTFEGGIKL	234
Oy		241	EIK 243	
Dd		235	EIK 237	
RESULT 2				
O9GYF0		PRELIMINARY;	PRT;	298 AA.
ID	O9GYF0			
AC	O9GYF0;			
DT	01-MAY-2000 (TREMBlrel. 13, Created)			
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)			
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)			
DE	CN 8 scfv.			
GN	CN 8.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.			
OX	NCBI_TaxID=10090;			
RA	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Balb/c; TISSUE=Spleen;			
RX	MEDLINE=20183931; PubMed=10706631;			
RT	Shinohara N., Demura T., Fukuda H.;			
RT	"Isolation of a vascular cell wall-specific monoclonal antibody			
RT	recognizing a cell polarity by using a phage display subtraction			
method."				
RL	Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).			
DR	EMBL; AB036341; BAA88633.1; -.			
DR	PIR; A33933; A33933.			
DR	PIR; S19112; S19112.			
DR	HSSP; P01607; IREI.			
DR	InterPro; IPRO07110; Ig-like.			
DR	InterPro; IPRO03596; Ig_v.			
DR	Pfam; PF00047; Ig_2.			
DR	SMART; SM00406; IGV; 2.			
DR	PROSITE; PS00835; IG-LIKE; 2.			
SQ	SEQUENCE 298 AA; 31867 MW; E0F96BBA17004317 CRC64;			
Query Match		54.0%; Score 696.5; DB 11; Length 298;		
Best Local Similarity		53.3%; Pred. No.1.le-49;		
Matches 131; Conservative 43; Mismatches 63; Indels 9; Gaps 3				
Oy		1	OYOLQOQSAGELVRSASVKLSTASGFENIKDYMMHWKRPBOGLFMIGWLPENGDTXY	60
		:::::	:::::	:::::
Dd		40	OYKLOQOQSGGGLVPKGSLILSCAAGSDPSRYVMGWVRQAPKPKGLEMGEINPDSTINY	99
		:::::	:::::	:::::
Oy		61	APKFGKAITMTADTSNTAYILOSSLASEDTAVVYC---NFYGDALDVWGCGTTVVSSG	117
		:::::	:::::	:::::
Dd		100	TPLSKDKPTLISDNMAKNITLYLQMSKYRSEDITLYLCARASYGHSA-YWGQGITTVVSSG	158
		:::::	:::::	:::::
Oy		118	GGSGGSGSGSGGSDVLMTOTPEPLLISVTITGPASPISCKSSQSLDSBGKTYYNWLLORPG	177
		:::::	:::::	:::::
Dd		159	GGSGGSGSGSGGSDIEILTQPASIASASVGFTVITTCRASGNI-----HNYLAWYOQXOG	213
		:::::	:::::	:::::
Oy		178	QSPKULIYIVSLDLSGVDPRTFGSGSGCTFTLKINRVAEDLIQVYWCQTHSPLTFGAG	237
		:::::	:::::	:::::
Dd		214	KSPOLLVYNAKTLADGVPSRFSGSGGTQYSLKINSLOPEDFSGYCQHFWTPPYTFGGG	273
		:::::	:::::	:::::
Oy		238	TKLEIK 243	
Dd		274	TKLEIK 279	
RESULT 3				
ID	O921A6	PRELIMINARY;	PRT;	241 AA.
AC	O921A6;			
DT	01-DEC-2001 (TREMBlrel. 19, Created)			

DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE	Anti-CEA 79 single chain Fv fragment (Fragment).
OS	Mus musculus (Mouse).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
EX	MEDLINE=96170165; PubMed=9509426;
RA	Chung Y.H., Choi S.J., Kim H.-J., Kim I.-J., Choi I.H., Lee S.D.,
RA	Yi K.S., Suh P.G., Ryu S.H., Chung H.K.?
RT	"Cloning and characterization of cDNAs encoding VH and VL of a
RT	monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT	generation of a single-chain Fv molecule (scFv).";
RL	Mol. Cells 7:816-819 (1997).
DR	EMBL; U88067; AAB48044.1; -
DR	InterPro; IPRO07119; IG-like.
DR	InterPro; IPRO03596; IG_v.
DR	Pfam; PF00047; Ig_2.
DR	SMART; SM00406; IGV_2.
DR	PROSITE; PS50835; IG_LIKE; 2.
FT	NON TER 1
FT	NON TER 241
SQ	SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;
Query Match	51.0%; Score 657; DB 11; Length 241;
Best Local Similarity	50.8%; Fred. No. 1.6e-46;
Matches 126; Conservative 45; Mismatches 63; Indels 14; Gaps 5;	
OY	1 QVQLQQSGAEELVRSGASVKLSCTASGKFIKPYYMHMWYKOREOGLWIGIDPENGDREY 60 :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Dd	1 QVQLQQSQPELAKRQEETLVICKSAGFTPTDYGMMWKQAQKGKLKMGMINTYTGEPLTY 60 QVQLQQSQPELAKRQEETLVICKSAGFTPTDYGMMWKQAQKGKLKMGMINTYTGEPLTY
OY	61 APKEGGATMTADITSSNTAVILQLSSLASEDPNAVYYCNFYGDAL--DYWGCGITYTVASSG 117 : ::
Dd	61 ADDEFGRAPAFSLNETSASTAYAIQNINLKNEPDATVFEC-ARKDLIRFDYWGGQTIVTVASSG 119 : ::
OY	118 GGSGSGSGSGSGGSYSVMTCQPPIILSVTIQGPAISICSSQSOLDSDSKTLNNMLIQRP 177 : ::
Dd	120 GGSGSGSGSGSGGSIELTQSPSSIASLGKVTTCVASQ----DIKKYLAMTGQRFG 174 : ::
OY	176 OSPKRLLVLKSDBGVPDFETGSGSGNDPFLIKLNRYVAEHLIGVYC--WOGTSHPLTFPG 235 : ::
Dd	175 KGPENAHHTLIHYIQGITPSRSRGSGSRDISFSISNLEPHDIAITYCLHYNLH---IFG 231 : ::
OY	236 AGTKLELRK 243 ::
Dd	232 GGTKLELRK 239 ::
RESULT 4	
ID	Q9Z5S1 PRELIMINARY; PRT; 218 AA.
AC	Q9Z5S1:
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	MRPs (Fragment).
OS	Mus musculus (Mouse).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/c;
RX	Pubmed=11819679;
RA	Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA	Su C.?
RT	"Mechanism of exogenous nucleic acids and their precursors improving
RT	the repair of intestinal epithelium after irradiation in mice.";
RL	World J. Gastroenterol. 6:709-717(2000).
RN	[2]

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RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain."
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; Ig_Like; 1.
DR NON_TER 218
SQ SEQUENCE 218 AA; 23013 MW; 5274FA8F7982817 CRC64;

Query Match 48.1%; Score 620.5; DB 11; Length 218;
Best Local Similarity 53.9%; Pred. No. 1,5e-43;
Matches 117; Conservative 44; Mismatches 53; Indels 3; Gaps 2;

QY 1 QVQLQSGAEIVSGASVKSCTASGPNIKDYVHWKORPROGLEWIGIDPENGDTLEY 60
DQ 3 QVQLQSGPELTKRGRTVRSCKASGTTTACGMQVQKMPGKLGKINITHSGVPKY 62
QY 61 APKFGKATMTADTSNTAVYLQLSLASEDTAVYCN--FYGDALDYWGQGTIVTSSGG 118
DQ 63 APKFGKRFAPSLTSTASTAVYLQISLNKNEDTATYFCMRMDYDGFAYWGQGTIVTSSGG 122
QY 119 GSGGGSGSGSGSDVMTQPTLTSTIGCPASISCKSSQLDSDGKTYLMLQRPQ 178
DQ 123 GSGGGSGSGSGSDIVLTQSPASLAVSLGGRATISGRASS--VDNIGISPMFVQKPPQ 181
QY 179 SPKRLIYIVSKLDSGVPDRFTSGSGTDFTLKINRYE 215
DQ 182 PKKLIYASKSGSGVPAGLLASGSDTDSINITYME 218

RESULT 5
Q99LJ31 PRELIMINARY; PRT; 468 AA.
ID Q99LJ31;
AC Q99LJ31;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, last annotation update)
DE Similar to RIKEN CDNA 181060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR PDB; 2AE2; 24-NOV-99.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; Ig_Like; 4.
DR PROSITE; PS50290; Ig_MHC; 1.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 40.5%; Score 522.5; DB 11; Length 468;
Best Local Similarity 83.2%; Pred. No. 5,2e-35;
Matches 99; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQSGAEIVSGASVKSCTASGPNIKDYVHWKORPROGLEWIGIDPENGDTLEY 60
DQ 20 EVQLQSGAEIVRPGASVSLSTASGPNIKDLSLMMHWKORPROGLEWIGIDPENGDTLEY 79
QY 61 APKFGKATMTADTSNTAVYLQLSLASEDTAVYCN--FYGDALDYWGQGTIVTSS 116

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DQ 80 APKFGKATMTADTSNTAVYLQLSLASEDTAVYCN--FYGDALDYWGQGTIVTSS 138

RESULT 6
Q8K122 PRELIMINARY; PRT; 148 AA.
ID Q8K122;
AC Q8K122;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028925; AAH28925.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PS50835; Ig_Like; 1.
KW Hypothetical protein.
SQ SEQUENCE 148 AA; 16345 MW; 183920BBD9F3B521 CRC64;

Query Match 39.6%; Score 511; DB 11; Length 148;
Best Local Similarity 97.0%; Pred. No. 1,1e-34;
Matches 97; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 132 DVAMTQPTLTSTIGOPASISCKSSQLDSDGKTYLMLQRPQSPKRLIYIVSKLD 191
DQ 20 DVAMTQPTLTSTIGOPASISCKSSQLDSDGKTYLMLQRPQSPKRLIYIVSKLD 79
QY 192 GGVPRFTSGSGTDFTLKINRYEADLGVYVQWQGTSP 231
DQ 80 GGVPRFTSGSGTDFTLKISVVEADLGVYVQWQGTSP 119

RESULT 7
Q8K0F8 PRELIMINARY; PRT; 239 AA.
ID Q8K0F8;
AC Q8K0F8;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031498; AAH31498.1; -.
DR PIR; A33933; A33933.
DR PDB; 1KN2; 13-MAR-02.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR003599; Ig_short.
DR InterPro; IPR007110; Ig_Like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.

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DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IG1; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Hypothetical protein.
 KW SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;

Query Match 38.6%; Score 497; DB 11; Length 239;
 Best Local Similarity 86.8%; Pred. No. 2.8e-33;
 Matches 97; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 132 DVMTQTPLTSLVITIGQPASISCKSSQSLSDSGKTYLNMILORPGSPKRLIYVSKLD 191
 DB 21 DVMTQTPLTSLVITIGQPASISCKSSQSLFTNGKMYLSLILGRPGSPKRLIYVSKLD 80
 QY 192 SGVPDRFTSGSGGSDFTLTKINRYEADLGYIYCWGTHSPITGAGTKLEIK 243
 DB 81 SGVPDRFTSGSGGSDFTLTKINRYEADLGYIYCLQSTHPTFGGTKLEIK 132

RESULT 8
 Q8TCD0 PRELIMINARY; PRT; 239 AA.

AC Q8TCD0;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022362; AAH22362.1; -
 DR PIR; S34095; S34095.
 DR PIR; S42267; S42267.
 DR PIR; S42268; S42268.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26234 MW; FACEDC3AJB03871D CRC64;

Query Match 36.6%; Score 472; DB 4; Length 239;
 Best Local Similarity 76.78%; Pred. No. 3.4e-31;
 Matches 89; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

QY 128 GGSQDVMTQTPLTSLVITIGQPASISCKSSQSLSDSGKTYLNMILORPGSPKRLIYLV 187
 DB 17 GGSQDVMTQTPLTSLVITIGQPASISCKSSQSLVSDNTYLNLFQGRPGSPKRLIYKV 76
 QY 188 SKLDSGVDRFTSGSGGSDFTLTKINRYEADLGYIYCWGTHSPITGAGTKLEIK 243
 DB 77 SNRDSGVDRFTSGSGGSDFTLTKINRYEADLGYIYFQWQTHWPSTFGGTKLEIK 132

RESULT 9
 Q925S2 PRELIMINARY; PRT; 170 AA.
 ID Q925S2;
 AC Q925S2;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE MRP4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA PubMed=11819679;
 RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
 RA Su C.;
 RT "Mechanism of exogenous nucleic acids and their precursors improving
 the repair of intestinal epithelium after irradiation in mice."
 RL World J. Gastroenterol. 6:709-717(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Cui D., Zeng G., Yan X., Li X., Su C.;
 RT "Cloning of mouse genes related to repairing of intestinal epithelium
 of the irradiated mice by treatment with the intestinal RNA of mice of
 the same strain."
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
 DR EMBL; AF240167; AAK43732.1; -
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 SQ SEQUENCE 170 AA; 17978 MW; 50428230C6C10F38 CRC64;

Query Match 34.9%; Score 450.5; DB 11; Length 170;
 Best Local Similarity 62.8%; Pred. No. 1.3e-29;
 Matches 86; Conservative 16; Mismatches 30; Indels 5; Gaps 2;

QY 1 QVQLQSGAEIVSGASVYKLSCTASGFNIDYMMHWKORPEQGLEWIGDPEVDTEY 60
 DB 3 QVQLQSGPEVPAAGVSVKISCKSGYTFDYEMHWKMMHQAOSLWIGIISTYDQNTNY 62
 QY 61 APTFOGKAMTATTSNSTALQISLASRDTAYYC--NFYED--ALDWGGQTVYTVS 115
 DB 63 NQKFKGKMTVTKSSITAYMELARLTSDSAIYGCARGAVYSFYFDYWGQCTVTVS 122
 QY 116 SGGGSGSGGSGGGGSD 132
 DB 123 SGGGSGSGGSGGGGSD 139

RESULT 10
 Q99W37 PRELIMINARY; PRT; 238 AA.

AC Q99W37;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC002035; AAH02035.1; -
 DR PIR; A31807; A31807.
 DR PIR; A32248; A32248.
 DR PIR; B32248; B32248.
 DR PIR; C32248; C32248.
 DR PIR; F32530; F32530.
 DR PIR; PH1042; PH1042.
 DR PIR; PH1043; PH1043.
 DR PIR; PH1044; PH1044.


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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/c; PubMed:10992488;
RA Makiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL: AF206021; AAF69319.1; -.
DR HSSP: P01810; 2FBU.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CED4EDE CRC64;

Query Match 34.4%; Score 443.5; DB 11; Length 109;
Best Local Similarity 78.9%; Pred. No. 2.8e-29;
Matches 86; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

QY 9 AELVRSGAVKLSCTASGFIKDYMHVWVQKPEQGLEWIGMIDPENGDTEYAPKQGA 68
Db 1 AELVKGASVKTLSCTASGFNIETDMVWVQKPEQGLEWIGRIDPAHGSHKYPKFGKA 60

QY 69 TMTADTSSNTAYQLSLASEDTAVVYCNFYDAL-DYMGQTTVYSS 116
Db 61 TITSSTSSNTAYQLSLTSEDVAVVYCVRRGAVFDMGQGTALTVSS 109

RESULT 14
Q8VC16 PRELIMINARY; PRT; 238 AA.
ID Q8VC16
AC Q8VC16;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Straubberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC019760; AAH19760.1; -.
DR PIR: A27887; A27887.
DR PIR: A32248; A32248.
DR PIR: A33933; A33933.
DR PIR: B27887; B27887.
DR PIR: B30577; B30577.
DR PIR: B31485; B31485.
DR PIR: B32248; B32248.
DR PIR: B41940; B41940.
DR PIR: C27887; C27887.
DR PIR: C32248; C32248.
DR PIR: C34904; C34904.
DR PIR: D27887; D27887.
DR PIR: D29380; D29380.
DR PIR: E28833; E28833.
DR PIR: F32530; F32530.
DR PIR: H31485; H31485.
DR PIR: PH0106; PH0106.
DR PIR: PH1030; PH1030.
DR PIR: PH1031; PH1031.
DR PIR: PH1034; PH1034.

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DR PIR: PL0257; PL0257.
DR PIR: PT0359; PT0359.
DR PIR: S07435; S07435.
DR PIR: S16112; S16112.
DR PIR: S26334; S26334.
DR PIR: S53750; S53750.
DR PIR: S60066; S60066.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_2.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35BC08B3DE5414AD CRC64;

Query Match 34.0%; Score 438; DB 11; Length 238;
Best Local Similarity 75.2%; Pred. No. 2.2e-28;
Matches 85; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 131 SVTLMTQTLETLTYTIGQPASISCKSSQSILSDGKTYNMLHPRGQSPKRLIYVSKL 190
Db 19 SDVVMQTPLSPVSGDQASISCKSSQSLVHNSNTYIHWIQRKGQSPKRLIYVSKN 78

QY 191 DSGVPRFTSGSGGTFTLKINRVEAEDLVGYVYCWGTHSPITFGATKLEIK 243
Db 79 FSGVPRFTSGSGGTFTLKISRVEAEDLVGYVYCWGTHSPITFGATKLEIK 131

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RESULT 15
Q924P9 PRELIMINARY; PRT; 143 AA.
ID Q924P9
AC Q924P9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE V303-D-J-C mu protein (Fragment).
DN V303-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB069916; BAB63932.1; -.
DR PIR: PH1161; PH1161.
DR PIR: PH1162; PH1162.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 143 AA; 15704 MW; 43CD8C72D52134FE CRC64;

Query Match 33.7%; Score 435; DB 11; Length 143;
Best Local Similarity 70.3%; Pred. No. 2e-28;
Matches 83; Conservative 13; Mismatches 20; Indels 2; Gaps 1;

QY 1 QVQLQSGAEIVRSGAVKLSCTASGFIKDYMHVWVQKPEQGLEWIGMIDPENGDTEY 60
Db 1 QVQLQGLAEIVKPGASVKTLSCTASGFNIETDMVWVQKPEQGLEWIGIDPSDYNY 60

QY 61 APKFGKATMTADTSSNTAYQLSLASEDTAVVYCNFYDAL-DYMGQTTVYSS 116
Db 61 TITSSTSSNTAYQLSLTSEDVAVVYCVRRGAVFDMGQGTALTVSS 109

```

Db 61 N0KEKATLTVDTSSTAYM0LSLTFSEDSAVYYCASHYYGSSDYWG0GTTLTWSS 118

Search completed: July 30, 2004, 11:21:08
Job time : 35.5732 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 30, 2004, 11:14:51 ; Search time 49.0915 Seconds

(without alignments)
1433.128 Million cell updates/sec

Title: US-09-297-181-4

Sequence: 1 QVRLQSGALVRSAGSVNL.....YCKQSYNLPFGGKLEIK 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003ps:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1315	100.0	249	2	AAW60770
2	1024.5	77.9	288	2	AAW82743
3	1024.5	77.9	673	2	AAW82742
4	961	73.1	243	2	AAW60769
5	955	72.6	535	2	AAW28491
6	955	72.6	535	2	AAW28492
7	951	72.3	580	2	AAW90217
8	942	71.6	556	2	AAW90218
9	932.5	70.9	437	2	AAW37738
10	931	70.8	258	5	AAU72865
11	930	70.7	248	2	AAU72865
12	924.5	70.3	240	6	AAU72865
13	923.5	70.2	242	4	AAU72865
14	921	70.0	248	2	AAU72865
15	917.5	69.8	238	5	AAU72865
16	917.5	69.8	238	5	AAU72865
17	917.5	69.8	238	5	AAU72865
18	913.5	69.5	240	5	AAU72865
19	913.5	69.5	240	5	AAU72865
20	913.5	69.5	240	5	AAU72865
21	906	68.9	262	4	AAU72865
22	906	68.9	262	4	AAU72865
23	906	68.9	262	4	AAU72865
24	905.5	68.9	238	5	AAU72865
25	904	68.7	241	7	AAU72865

26	901	68.5	248	2	AAU72865
27	899	68.4	240	7	AAU72865
28	897	68.2	271	4	AAU72865
29	896.5	68.2	272	4	AAU72865
30	891	67.8	500	7	AAU72865
31	889.5	67.6	258	5	AAU72865
32	883.5	67.2	258	5	AAU72865
33	883.5	67.2	258	5	AAU72865
34	883.5	67.2	258	5	AAU72865
35	883	67.1	270	2	AAU72865
36	882.5	67.1	258	5	AAU72865
37	882.5	67.1	258	5	AAU72865
38	880	66.9	258	5	AAU72865
39	879.5	66.9	258	5	AAU72865
40	879	66.8	444	6	AAU72865
41	879	66.8	556	4	AAU72865
42	877.5	66.7	282	2	AAU72865
43	877.5	66.7	282	2	AAU72865
44	877	66.7	553	2	AAU72865
45	877	66.7	553	2	AAU72865

ALIGNMENTS

RESULT 1
AAW60770
ID AAW60770 standard; protein; 249 AA.
XX
AC AAW60770;
XX
DT 08-SEP-1998 (first entry)
XX
DE Single chain antibody (ScFv) D3M that binds to mutant p53 proteins.
XX
KW Single chain antibody; ScFv D3M; mouse; p53 protein; oligomerisation;
KW regulatory domain; p53 mutant; H273; W248; G281;
KW p53-dependent trans-activating activity; restoration;
KW tumour-suppressing activity; tumour cell; treatment; hyper-proliferation;
KW cancer; re-stenosis; ss.
XX
OS Mus sp.
XX
PN W09818825-A1.
XX
PD 07-MAY-1998.
XX
PF 27-OCT-1997; 97WO-FR001921.
XX
PR 29-OCT-1996; 96FR-00013176.
XX
PA (RHON) RHONE-POULENC RORER SA.
XX
PI Bracco L, Debussche L;
XX
DR WPI: 1998-272140/24.
XX
N-PSDB: AAV36237.
XX
PT Restoring p53-dependent trans-activating activity to cell containing
PT mutant p53 - by delivering single-chain antibody specific for the mutant,
PT particularly for treatment of tumours.
XX
PS Claim 5; Page 32; 54pp; French.
XX
CC The present sequence represents a single chain antibody (ScFv) designated
CC D3M. The antibody binds to an epitope present in the C-terminal region of
CC the p53 protein that includes oligomerisation and regulatory domains,
CC specifically between positions 320 and 393. ScFv D3M is directed against
CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is
CC introduced into cells containing a mutant p53 protein, p53-dependent
CC trans-activating activity is restored. ScFv D3M is specific for p53-
CC mutants that have lost tumour-suppressing activity and are present in
CC tumour cells. It is particularly used to treat hyper-proliferation

CC associated with these mutants (e.g. cancer and re-stenosis) but may also
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant
 CC and to purify or detect p53

XX Sequence 249 AA;

Query Match 100.0%; Score 1315; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 1,4e-87;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSSGAEIVRSGASVNLSTASGFNFKDYMMHWKQRPREGLMIGYIDPESGETEY 60
 DB 1 QVQLQSSGAEIVRSGASVNLSTASGFNFKDYMMHWKQRPREGLMIGYIDPESGETEY 60
 QY 61 APNFGQKATVYADTSNTAVLHLISLTSEDTYYVCNAVITYEYDGYALDYWGQGTIVY 120
 DB 61 APNFGQKATVYADTSNTAVLHLISLTSEDTYYVCNAVITYEYDGYALDYWGQGTIVY 120
 QY 121 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVMCKSSQSLFNSRTRKNYLAWYQ 180
 DB 121 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVMCKSSQSLFNSRTRKNYLAWYQ 180
 QY 181 QKPGQSPKVLITYMASTRSGVDPDRFTGSGSGTDFLTITISVQAEADLAIVYCKOSYNIPTF 240
 DB 181 QKPGQSPKVLITYMASTRSGVDPDRFTGSGSGTDFLTITISVQAEADLAIVYCKOSYNIPTF 240
 QY 241 GGGTKLEIK 249
 DB 241 GGGTKLEIK 249

RESULT 2

AAW82743 ID AAW82743 standard; protein; 288 AA.

XX AAW82743;

XX 10-MAY-1999 (first entry)

DE Fusion protein PNG4/55.lscFv/CPG2 R6/del EcorI.

XX Conjugate; cell targeting; cytotoxic drug; plasmid; fusion protein;
 KM producing-converting enzyme; cell surface antigen; treatment; cancer;
 KM inflammation; rheumatoid arthritis; antibody; produg therapy system.

XX Synthetic.

XX WO9851787-A2.

XX 19-NOV-1998.

XX 05-MAY-1998; 98WO-GB001294.

XX 10-MAY-1997; 97GB-00009421.

XX (ZENNE) ZENNECA LTD.

XX Emery SC, Blakey DC;

XX WPI, 1999-059700/05.

XX N-PSDB; AAV72064.

XX New gene construct expressing conjugate of targeting agent and produg-
 PT converting enzyme - useful for, e.g. targeted production of cytotoxic
 PT drug in vivo, especially for treatment of cancer.

XX Example 15; Page 82; 100pp; English.

XX This sequence is a used in a method for obtaining a novel gene construct
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-
 CC targeting group (I) and a heterologous produg-converting enzyme (II),
 CC and (B) is directed to leave the cell for selective localisation at a
 CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target

CC site, then administration of (III) is used for targeted release of
 CC cytotoxic drug, specifically for treating cancer but also inflammation
 CC such as rheumatoid arthritis. In situ generation of the targeting
 CC antibody increases selectivity, reducing side effects at normal tissue.
 CC The method is applicable to any antibody-directed enzyme produg therapy
 CC system

XX Sequence 288 AA;

Query Match 77.9%; Score 1024.5; DB 2; Length 288;
 Best Local Similarity 77.9%; Pred. No. 1.9e-66;
 Matches 194; Conservative 21; Mismatches 33; Indels 1; Gaps 1;

QY 1 QVQLQSSGAEIVRSGASVNLSTASGFNFKDYMMHWKQRPREGLMIGYIDPESGETEY 60
 DB 23 QVQLQSSGAEIVRSGASVNLSTASGFNFKDYMMHWKQRPREGLMIGYIDPESGETEY 82
 QY 61 APNFGQKATVYADTSNTAVLHLISLTSEDTYYVCNAVITYEYDGYALDYWGQGTIVY 120
 DB 61 APNFGQKATVYADTSNTAVLHLISLTSEDTYYVCNAVITYEYDGYALDYWGQGTIVY 141
 QY 83 NEFKKAKTLITVSKSTAYVMQLSLTSDSAVYYCARRAYGYD-ANDYWGQGTIVY 141
 DB 121 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVMCKSSQSLFNSRTRKNYLAWYQ 180
 QY 142 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVMCKSSQSLFNSRTRKNYLAWYQ 201
 DB 181 QKPGQSPKVLITYMASTRSGVDPDRFTGSGSGTDFLTITISVQAEADLAIVYCKOSYNIPTF 240
 QY 202 QKPGQSPKVLITYMASTRSGVDPDRFTGSGSGTDFLTITISVQAEADLAIVYCKOSYNIPTF 261
 DB 241 GGGTKLEIK 249
 QY 262 GGGTKLEIK 270

RESULT 3

AAW82742 ID AAW82742 standard; protein; 673 AA.

XX AAW82742;

XX 10-MAY-1999 (first entry)

DE Plasmid PNG4/55.lscFv/CPG2 R6 protein.

XX Conjugate; cell targeting; cytotoxic drug; produg-converting enzyme;
 KM cell surface antigen; treatment; cancer; inflammation; antibody;
 KM rheumatoid arthritis; produg therapy system.

XX Synthetic.

XX WO9851787-A2.

XX 19-NOV-1998.

XX 05-MAY-1998; 98WO-GB001294.

XX 10-MAY-1997; 97GB-00009421.

XX (ZENNE) ZENNECA LTD.

XX Emery SC, Blakey DC;

XX WPI, 1999-059700/05.

XX N-PSDB; AAV72059.

XX New gene construct expressing conjugate of targeting agent and produg-
 PT converting enzyme - useful for, e.g. targeted production of cytotoxic
 PT drug in vivo, especially for treatment of cancer.

XX Example 14; Page 78-79; 100pp; English.

XX This sequence is used in a method for obtaining a novel gene construct
 CC (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-

CC targeting group (I) and a heterologous prodrug-converting enzyme (II),
 CC and (B) is directed to leave the cell for selective localisation at a
 CC cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target
 CC site, then administration of (II) is used for targeted release of
 CC cytotoxic drug, specifically for treating cancer but also inflammation
 CC such as rheumatoid arthritis. In situ generation of the targeting
 CC antibody increases selectivity, reducing side effects at normal tissue.
 CC The method is applicable to any antibody-directed enzyme prodrug therapy
 CC system
 XX
 SQ Sequence 673 AA;
 Query Match 77.9%; Score 1024.5; DB 2; Length 673;
 Best Local Similarity 77.9%; Pred. No. 4.9e-66;
 Matches 194; Conservative 21; Mismatches 33; Indels 1; Gaps 1;
 QY 1 QVKLQESGAEIVNSGASVNLSTASGFNPKDYMHVWKORPEBGLMIGYIDPESGETEY 60
 Db 20 QVQLQSGAEIVNSGASVNLSTASGFNPKDYMHVWKORPEBGLMIGYIDPESGETEY 79
 QY 61 APNFGKAVTADTSSNTAYLHLSLTSEDTYYVCNAVYYEYDGYALDYWGQGTITVY 120
 Db 80 NEFKKAKLTIVKSSSTTAYMQSLTSEDSAYYCARERAYGD-AMDYWGQGTITVY 138
 QY 121 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVMCKSSQSLFNSRTKRYLAWYQ 180
 Db 139 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVMCKSSQSLNSTRKRYLAWYQ 198
 QY 181 QKPGSPKVLIVASTRESGVDPDRFTGSGSGTDFTLTSSVOAEDLAVYYCKSYNLPF 240
 Db 199 QKPGSPKVLIVASTRESGVDPDRFTGSGSGTDFTLTSSVOAEDLAVYYCKSYNLPF 258
 QY 241 GGGTKLEIK 249
 Db 259 GGGTKLEIK 267
 RESULT 4
 AAM60769
 ID AAM60769 standard; protein; 243 AA.
 AC AAM60769;
 XX
 DT 08-SEP-1998 (first entry)
 DE Single chain antibody (ScFv) 421 that binds to mutant p53 proteins.
 XX
 KW Single chain antibody; ScFv 421; mouse; p53 protein; oligomerisation;
 KW regulatory domain; p53 mutant; H273; W248; G281;
 KW p53-dependent trans-activating activity; restoration;
 KW tumour-suppressing activity; tumour cell; treatment; hyper-proliferation;
 KW cancer; re-stenosis; ss.
 XX
 OS Mus sp.
 XX
 PN WO9818825-A1.
 PD 07-MAY-1998.
 XX
 PF 27-OCT-1997; 97WO-FR001921.
 XX
 PR 29-OCT-1996; 96FR-00013176.
 XX
 PA (RHON) RHONE-POULENC RORER SA.
 XX
 PI Bracco I, Debussche L;
 XX
 DR WPT, 1998-272140/24.
 DR N-PSDB; AAV36236.
 XX
 PT Restoring p53-dependent trans-activating activity to cell containing
 PT mutant p53 - by delivering single-chain antibody specific for the mutant,
 PT particularly for treatment of tumours.

XX
 PS Claim 5; Page 31; 54pp. French.
 XX
 CC The present sequence represents a single chain antibody (ScFv) designated
 CC 421. The antibody binds to an epitope present in the C-terminal region of
 CC the p53 protein that includes oligomerisation and regulatory domains.
 CC Specifically between positions 320 and 393. ScFv 421 is directed against
 CC p53 mutants, particularly H273, W248 and G281 mutants. When the ScFv is
 CC introduced into cells containing a mutant p53 protein, p53-dependent
 CC trans-activating activity is restored. ScFv 421 is specific for p53-
 CC mutants that have lost tumour-suppressing activity and are present in
 CC tumour cells. It is particularly used to treat hyper-proliferation
 CC associated with these mutants (e.g. cancer and re-stenosis) but may also
 CC be used in vitro for studying mechanisms of activity of p53 or its mutant
 CC and to purify or detect p53
 XX
 SQ Sequence 243 AA;
 Query Match 73.1%; Score 961; DB 2; Length 243;
 Best Local Similarity 74.8%; Pred. No. 6.4e-62;
 Matches 187; Conservative 23; Mismatches 32; Indels 8; Gaps 3;
 QY 1 QVKLQESGAEIVNSGASVNLSTASGFNPKDYMHVWKORPEBGLMIGYIDPESGETEY 60
 Db 1 QVQLQSGAEIVNSGASVNLSTASGFNPKDYMHVWKORPEBGLMIGYIDPESGETEY 60
 QY 61 APNFGKAVTADTSSNTAYLHLSLTSEDTYYVCNAVYYEYDGYALDYWGQGTITVY 120
 Db 61 APNFGKAVTADTSSNTAYLHLSLTSEDTYYVCNAVYYEYDGYALDYWGQGTITVY 114
 QY 121 SSGGGSGGGSGGGSDIELTQSPSLAVSAGEKVMCKSSQSLFNSRTKRYLAWYQ 180
 Db 115 SSGGGSGGGSGGGSDIVLMTQTPLTSLTGGPASIACKSSQSLDS-DGTYTNNMLL 173
 QY 181 QKPGSPKVLIVASTRESGVDPDRFTGSGSGTDFTLTSSVOAEDLAVYYCKSYNLPF 239
 Db 174 QKPGSPKVLIVASTRESGVDPDRFTGSGSGTDFTLTSSVOAEDLAVYYCKSYNLPF 233
 QY 240 FGGTKLEIK 249
 Db 234 FGGTKLEIK 243
 RESULT 5
 AAM28491
 ID AAM28491 standard; protein; 535 AA.
 AC AAM28491;
 XX
 DT 25-NOV-1997 (first entry)
 DE Human p53 protein variant S-325 encoded by p5C176.
 XX
 KW Leucine zipper domain; LZD; oligomerisation domain; mutant; muten;
 KW subcutaneous; replacement; transactivation; viral protein VP16; HSV,
 KW anti-oncogene; hyperproliferation; cancer; re-stenosis; ScFv;
 KW tumour suppression; apoptosis; single chain antibody variable domain.
 XX
 OS Homo sapiens.
 OS Herpes simplex virus.
 OS Synthetic.
 OS Chimeric.
 XX
 PN WO9704092-A1.
 PD 06-FEB-1997.
 XX
 PF 17-JUL-1996; 96WO-FR001111.
 XX
 PR 19-JUL-1995; 95FR-00008729.
 XX
 PA (RHON) RHONE POULENC RORER SA.

PI Conseller E, Bracco L;
 XX
 DR MPI: 1997-132633/12.
 DR N-PSDB; AAT86221.
 XX
 PT New p53 variants e.g. with oligomerisation domain replaced by leucine
 PT zipper - useful for treating hyper-proliferative disorders, esp. cancer
 PT and restenosis.
 XX
 PS Claim 36; Page 88-90; 133pp; French.
 CC Claimed variants of protein p53 have at least part of the oligomerisation
 CC domain deleted and replaced by a leucine zipper domain. The mutants
 CC preferably also have at least part of the p53 transactivation domain
 CC (amino acids 1-74) deleted and replaced by the transactivating domain
 CC (TAD) from herpes simplex virus viral protein VP16 (amino acids 411-490)
 CC or by a protein domain able to bind selectively to a transactivator,
 CC especially a single-chain antibody variable domain (ScFv). The present
 CC sequence is that of a specifically claimed p53 variant designated S-325
 CC and comprising a ScFv domain, amino acids 75-325 of human wild-type p53
 CC and a leucine zipper domain at the C-terminal. The p53 variants are more
 CC active and more stable tumour suppressors and apoptosis-inducing agents
 CC than wild-type p53 and are active where the wild-type protein is not,
 CC i.e. they are not inactivated by dominant negative or oncogenic mutants,
 CC nor by other cellular proteins (because the leucine zipper domain
 CC prevents formation of inactive mixed oligomers)
 CC
 XX Sequence 535 AA;
 SQ
 Query Match 72.6%; Score 955; DB 2; Length 535;
 Best Local Similarity 74.4%; Pred. No. 4.1e-61;
 Matches 186; Conservative 23; Mismatches 33; Indels 8; Gaps 3;
 QY 1 QVKLOESGAEIVSGASVNLCTASGPNIKDYHAWKORPEEGLEWIGYIDPESGETEY 60
 Db 3 QVQLQESGAEIVSGASVNLCTASGPNIKDYHAWKORPEEGLEWIGYIDPESGETEY 62
 QY 61 APNFQKATVTADTSSNTAVYHLSLTSEDTTYYCNAVYYEYDGYALDYWGQGTITVY 120
 Db 63 APKFOKATVTADTSSNTAVYHLSLTSEDTTYYCNAVYYEYDGYALDYWGQGTITVY 116
 QY 121 SSGGGSGGGSGGGSGGSDIELTQSPSSLAAGKVMCKSSQSLNSFRKXYLAAYQ 180
 Db 117 SSGGGSGGGSGGGSGGSDVLTQTPPLTSLVTIGQPAISICKSSQSLDS-DGKTYLWML 175
 QY 181 QKPGQSPKVLITWMASTRESGVDPDRFTSGSGTDFTLTITSSVQADFLAVYYCKQSNLP-T 239
 Db 176 QRPQSPKRLITLVSKLDSGVDPDRFTSGSGTDFTLTINRVAEDLIGVYCMQGTHTSPLT 235
 QY 240 FGGGTKELEIK 249
 Db 236 FGAETKELEIK 245
 RESULT 6
 AAM28492
 ID AAM28492 standard; protein, 535 AA.
 AC AAM28492;
 XX
 DT 25-NOV-1997 (first entry)
 DE Human p53 protein variant S-325H.
 XX
 KW Leucine zipper domain; LZD; oligomerisation domain; mutant; mutein;
 KW substitution; replacement; transactivation; viral protein VP16; HSV;
 KW anti-oncogene; hyperproliferation; cancer; restenosis; ScFv;
 KW tumour suppression; apoptosis; single chain antibody variable domain.
 XX
 OS Homo sapiens.
 OS Herpes simplex virus.
 OS Synthetic.
 OS Chimeric.

XX
 FH Key Location/Qualifiers
 FT Misc-difference 361
 FT /note= "Arg residue at position 182 of wild-type p53 has
 FT been mutated to His"
 FT
 XX MO9704092-A1.
 XX
 XX 06-FEB-1997.
 XX
 XX 17-JUL-1996; 96WO-FR001111.
 XX
 XX 19-JUL-1995; 95FR-00008729.
 XX
 XX (RHON) RHONE POUJENC RORER SA.
 XX
 XX Conseller E, Bracco L;
 XX
 DR MPI: 1997-132633/12.
 XX
 PT New p53 variants e.g. with oligomerisation domain replaced by leucine
 PT zipper - useful for treating hyper-proliferative disorders, esp. cancer
 PT and restenosis.
 XX
 PS Claim 36; Page 133pp; French.
 CC Claimed variants of protein p53 have at least part of the oligomerisation
 CC domain deleted and replaced by a leucine zipper domain. The mutants
 CC preferably also have at least part of the p53 transactivation domain
 CC (amino acids 1-74) deleted and replaced by the transactivating domain
 CC (TAD) from herpes simplex virus viral protein VP16 (amino acids 411-490)
 CC or by a protein domain able to bind selectively to a transactivator,
 CC especially a single-chain antibody variable domain (ScFv). The present
 CC sequence is that of a specifically claimed p53 variant designated S-325H
 CC and comprising a ScFv domain, amino acids 75-325 of human wild-type p53
 CC (but with Arg182 replaced by His) and a leucine zipper domain at the C-
 CC terminal. The p53 variants are more active and more stable tumour
 CC suppressors and apoptosis-inducing agents than wild-type p53 and are
 CC active where the wild-type protein is not, i.e. they are not inactivated
 CC by dominant negative or oncogenic mutants, nor by other cellular proteins
 CC (because the leucine zipper domain prevents formation of inactive mixed
 CC oligomers). (Note: this sequence does not appear in the specification and
 CC has been produced by modifying the given sequence of variant V-325)
 CC
 XX Sequence 535 AA;
 SQ
 Query Match 72.6%; Score 955; DB 2; Length 535;
 Best Local Similarity 74.4%; Pred. No. 4.1e-61;
 Matches 186; Conservative 23; Mismatches 33; Indels 8; Gaps 3;
 QY 1 QVKLOESGAEIVSGASVNLCTASGPNIKDYHAWKORPEEGLEWIGYIDPESGETEY 60
 Db 3 QVQLQESGAEIVSGASVNLCTASGPNIKDYHAWKORPEEGLEWIGYIDPESGETEY 62
 QY 61 APNFQKATVTADTSSNTAVYHLSLTSEDTTYYCNAVYYEYDGYALDYWGQGTITVY 120
 Db 63 APKFOKATVTADTSSNTAVYHLSLTSEDTTYYCNAVYYEYDGYALDYWGQGTITVY 116
 QY 121 SSGGGSGGGSGGGSGGSDIELTQSPSSLAAGKVMCKSSQSLNSFRKXYLAAYQ 180
 Db 117 SSGGGSGGGSGGGSGGSDVLTQTPPLTSLVTIGQPAISICKSSQSLDS-DGKTYLWML 175
 QY 181 QKPGQSPKVLITWMASTRESGVDPDRFTSGSGTDFTLTITSSVQADFLAVYYCKQSNLP-T 239
 Db 176 QRPQSPKRLITLVSKLDSGVDPDRFTSGSGTDFTLTINRVAEDLIGVYCMQGTHTSPLT 235
 QY 240 FGGGTKELEIK 249
 Db 236 FGAETKELEIK 245
 RESULT 7
 AAM90217

ID AAM90217 standard; protein; 580 AA.
 XX AAM90217;
 AC
 XX 10-MAY-1999 (first entry)
 DT
 DE Bispecific tetraivalent antibody B1TAB7-24-IG10H6.
 XX
 KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
 KW T cell activation; inhibitor; graft versus host disease;
 KW transplant rejection; allograft rejection; autoimmune disease; allergy;
 KW therapy; human; bispecific tetraivalent antibody; B1Tab;
 KW B1TAB7-24-IG10H6.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key
 FT Peptide
 FT 1..24
 FT /note= "peB signal peptide"
 FT Region
 FT 25..138
 FT /note= "VH region anti B7.1 Mab"
 FT Peptide
 FT 139..153
 FT /note= "(G4S3) flexible linker"
 FT Region
 FT 154..262
 FT /note= "VL region anti B7.1 Mab"
 FT Misc-difference
 FT 261
 FT /note= "encoded by CTG"
 FT Region
 FT 263..273
 FT /note= "human IgG3 hinge region"
 FT Domain
 FT 274..308
 FT /note= "helix-turn-helix dimerisation domain"
 FT Domain
 FT 309..319
 FT /note= "human IgG3 hinge domain"
 FT Region
 FT 320..446
 FT /note= "VH region anti B7.2 Mab"
 FT Misc-difference
 FT 322..327
 FT /note= "codons for these amino acids are not present in the DNA sequence for B1TAB7-24-IG1-H6 provided in the specification"
 FT Peptide
 FT 447..461
 FT /note= "(G4S3) flexible linker"
 FT Region
 FT 462..574
 FT /note= "VL region anti B7.2 Mab"
 FT Peptide
 FT 575..580
 FT /note= "His6 tag"
 FT
 XX
 FN W09858965-A2.
 PD 30-DEC-1998.
 XX
 XX 22-JUN-1998; 98WO-EP003791.
 XX
 PR 20-JUN-1997; 97EP-00870092.
 XX
 XX (INNO-) INNOGENETICS NV.
 PA
 XX
 PI Lotte K, Sablon E, Buyse M, Bosman A;
 XX
 DR WPI; 1999-105615/09.
 DR N-PSDB; AAX01651.
 XX
 FT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
 FT immune diseases including allograft rejection.
 XX
 PS Example 7.1; Fig 16; 182pp; English.
 XX
 CC This polypeptide comprises the bispecific tetraivalent antibody B1TAB7-24
 CC -101016. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2
 CC anti B7.2 scFvs (tetravalency). One single B1Tab is a homodimer of 2
 CC identical molecules, each containing both an anti B7.1 and anti B7.2 scFv

CC (bispecificity). An anti-B7.1 and anti-B7.2 scFv are linked using a
 CC dimerisation domain (see AAM90219), which drives the homodimerisation of
 CC the molecule. DNA (see AAM01651) encoding the B1Tab has been constructed
 CC to allow expression of the B1Tab in transformed E. coli cells. The B1Tab
 CC cross-links, and/or cross-reacts, with the costimulatory molecules B7.1
 CC and B7.2 that are expressed on the membrane of professional antigen-
 CC presenting cells, leading to the inhibition of antigen-specific T cell
 CC activation. The invention relates to such B7-binding molecules, methods
 CC for their production, and their use for treating or preventing diseases
 CC of the immune system, in particular graft rejection, graft versus host
 CC disease, allergy and autoimmune diseases (claimed)
 CC
 XX
 SQ Sequence 580 AA:
 Query Match 72.3%; Score 951; DB 2; Length 580;
 Best Local Similarity 73.5%; Pred. No. 8,8e-61;
 Matches 183; Conservative 22; Mismatches 44; Indels 0; Gaps 0;
 QY 1 QVKLQESGAEIVRSGASVNLSTASGFNIKDYVMHWKQRPDEGLEWIGYIDPESGETEY 60
 DB 325 QVQLQSGPELEKFGASVKISKASGYSPFTCHNMNMWKQSKGLWMTGIIDPYGGSIX 384
 QY 61 APNFQKATVTADTSSNTAVLHLSLTSEDFTYVCNAVITYEYDGYALDYWGQGTIVTV 120
 DB 385 NPKFEGKATLTVDKSSSTAVWQLESLTSEDSAVYYCARFAYVGDYYIMDYWGQGTIVTV 444
 QY 121 SSGGGSGGGSGGGSGGSDIELTQSPSSLAWSAGEVMTCKSSQSVLSSNQNYLAWYQ 180
 DB 445 SSGGGSGGGSGGGSGGSDIELTQSPSSLAWSAGEVMTCKSSQSVLSSNQNYLAWYQ 504
 QY 181 QKPGQSPKVLITWASTRESGVDPFRFTSGSGTDEFTLTITSSVOADLNAVYYCKQSYNLPF 240
 DB 505 QKPGQSPKVLITWASTRESGVDPFRFTSGSGTDEFTLTITSSVOADLNAVYYCHQLSSWTF 564
 QY 241 GGGTKLRIRK 249
 DB 565 GGGTKLRIRK 573
 RESULT 8
 AAM90218
 ID AAM90218 standard; protein; 556 AA.
 XX
 AC AAM90218;
 XX
 DT 10-MAY-1999 (first entry)
 XX
 DE Bispecific tetraivalent antibody B1TAB1G10-B7-24H6.
 XX
 KW B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86;
 KW T cell activation; inhibitor; graft versus host disease;
 KW transplant rejection; allograft rejection; autoimmune disease; allergy;
 KW therapy; human; bispecific tetraivalent antibody; B1Tab;
 KW B1TAB1G10-B7-24H6.
 XX
 XX Mus sp.
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 OS
 FH Key
 FT Region
 FT Peptide
 FT 1..120
 FT /note= "VH region anti B7.2 Mab"
 FT Region
 FT 121..135
 FT /note= "(G4S3) flexible linker"
 FT Region
 FT 136..248
 FT /note= "VL region anti B7.2 Mab"
 FT Region
 FT 249..259
 FT /note= "human IgG3 hinge region"
 FT Domain
 FT 260..285
 FT /note= "helix-turn-helix dimerisation domain"
 FT Domain
 FT 286..305
 FT /note= "human IgG3 hinge domain"

FT Region 306..426
FT /note="VH region anti B7.1 Mab"
FT Peptide 427..441
FT /note=" (G4S3) flexible linker"
FT Region 442..550
FT /note="VL region anti B7.1 Mab"
FT Peptide 551..556
FT /note="His6 tag"
FN WO9658965-A2.
XX 30-DEC-1998.
XX
XX
XX 22-JUN-1998; 98WO-BP003791.
XX PF
XX 20-JUN-1997; 97EP-00870092.
XX PR
XX (INNO-) INNOGENETICS NV.
XX PA
XX Lorre K, Sablon E, Buysse M, Bosman A;
XX PI WPI; 1999-105615/09.
XX DR N-PSDB; AAX01652.
PT New molecules which bind B7.1 and B7.2 - useful to prevent and treat
PT immune diseases including allograft rejection.
XX
XX Example 7.1; Fig 18; 182pp; English.

XX This polypeptide comprises the bispecific tetraivalent antibody B17b1G10-
CC B7-24H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2
CC anti B7.2 scFvs (tetravalency). One single B17b is a homodimer of 2
CC identical molecules, each containing both an anti B7.1 and anti B7.2 scFv
CC (bispecificity). An anti-B7.1 and anti-B7.2 scFv are linked using a
CC dimerisation domain (see AAM90219), which drives the homodimerisation of
CC the molecule. DNA (see AAX01652) encoding the B17b has been constructed
CC to allow expression of the B17b in transformed E. coli cells. The B17b
CC cross-links, and/or cross-reacts, with the costimulatory molecules B7.1
CC and B7.2 that are expressed on the membrane of professional antigen-
CC presenting cells, leading to the inhibition of antigen-specific T cell
CC activation. The invention relates to such B7-binding molecules, methods
CC for their production, and their use for treating or preventing diseases
CC of the immune system, in particular graft rejection, graft versus host
CC disease, allergy and autoimmune diseases (claimed)

XX Sequence 556 AA;

Query Match 71.6%; Score 942; DB 2; Length 556;

Best Local Similarity 73.3%; Pred. No. 3.8e-60;
Matches 181; Conservative 22; Mismatches 44; Indels 0; Gaps 0;

QY 3 KLOESGAEIVRSAGASVNLSTASGFNIKDYMHWMKORPEGLMWTGYIDPESGTEYAP 62
DB 1 QLOESGAEIVRSAGASVNLSTASGFNIKDYMHWMKORPEGLMWTGYIDPESGTEYAP 60
QY 63 NFOGATVATADSSNNAVYHLSTSEPTTVYVCNAVITYEYGYALDWYGGTIVTVSS 122
DB 61 KRGKATITLVDSSTNAVYQLSTSEDSAVYICARFAVYGYITIMYWGQITIVTVSS 120
QY 123 GGGGGGGGGGGGGSDIELTQSPSSILAVSAGEKVMSCSSQSLFNSRTKRYLAWYQOK 182
DB 121 GGGGGGGGGGGGGSDIELTQSPSSILAVSAGEVMTCKSSQSVLYSSNQKRYLAWYQOK 180
QY 183 PGOSPKVLIYMASTESGVDRFTSGSGTDFLTITSSVOAEDLAVYCKQSYNLPTRGG 242
DB 181 PGOSPKVLIYMASTESGVDRFTSGSGTDFLTITSSVOAEDLAVYCHQYGLSSWTRGG 240
QY 243 GTKLEIK 249
DB 241 GTKLEIK 247

RESULT 9

AAM37738
ID AAM37738 standard; protein; 437 AA.

XX AAM37738;

AC 17-OCT-2003 (revised)

DT 07-JUL-1998 (first entry)

DE Nucleotide sequence encoding the Mgr6-clavin immunotoxin.

XX Recombinant ribosomal inhibitor protein; RIP; clavin; inhibition;
XX protein synthesis; conjugate; Mgr6-clavin; anticancer; antiviral agent.

OS Aspergillus clavatus.

OS Mus musculus.

OS Chimeric.

FT Key

FT Peptide Location/Qualifiers
FT /note="Mgr6 from M. musculus"
FT Peptide 287..437
FT /note="Clavin from A. clavatus"

XX WO9749726-A1.

XX 31-DEC-1997.

XX 26-JUN-1997; 97WO-BP003359.

XX 27-JUN-1996; 96IT-FI000155.

XX (ITV-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.

XX Mele A, De Santis R, Parente D, Cologhi M;

XX WPI; 1998-077109/07.

XX N-PSDB; AAV09256.

XX DNA encoding Aspergillus clavatus-derived ribosomal inhibitor protein,
XX clavin - useful as an immuno-conjugate and for treatment of cancer.

XX Claim 4; Page 14-15; 26pp; English.

XX This is the amino acid sequence of a fusion protein comprising of the Mgr6
XX single chain antibody (with the heavy and light chain joined by a
XX linker), fused to the clavin protein. Clavin is an inhibitor protein, and
XX functions by inactivating the ribosomes. Clavin or its conjugates are
XX useful as anticancer and/or antiviral agents. The recombinant ribosomal
XX inhibitor protein (RIP), Mgr6-clavin (a conjugate of clavin) is used as
XX an immunocjugate, and the complex and clavin alone are capable of
XX inhibiting ribosomal activity. (Updated on 17-OCT-2003 to standardise OS
XX field)

XX Sequence 437 AA;

Query Match 70.9%; Score 932.5; DB 2; Length 437;

Best Local Similarity 72.8%; Pred. No. 1.4e-59;
Matches 182; Conservative 25; Mismatches 36; Indels 7; Gaps 4;

QY 1 QYKLOESGAEIVRSAGASVNLSTASGFNIKDYMHWMKORPEGLMWTGYIDPESGTEY 60
DB 37 QYQLOESGAEIVRSAGASVNLSTASGFNIKDYMHWMKORPEGLMWTGYIDPESGTEY 96
QY 61 APNFGKATVADSSNNAVYHLSTSEPTTVYVCNAVITYEYGYALDWYGGTIVTV 120
DB 97 DPKFGKATITLVDSSTNAVYQLSTSEDSAVYICARFAVYGYITIMYWGQITIVTV 152
QY 121 SSGGGGGGGGGGGSDIELTQSPSSILAVSAGEKVMSCSSQSLFNSRTKRYLAWYQ 180
DB 153 SSGGGGGGGGGGGSDIELTQSPSSILAVSAGEKVMSCSSQSLFNSRTKRYLAWYQ 210
QY 181 QKPGOSPKVLIYMASTESGVDRFTSGSGTDFLTITSSVOAEDLAVYCKQSYNLP-T 239
DB 181 QKPGOSPKVLIYMASTESGVDRFTSGSGTDFLTITSSVOAEDLAVYCHQYGLSSWTRGG 240

Db 211 QKGPPLIKYASNLBSGVAPRPSGGSGTDFLTINHPVEDTATYYCOHSWEIPRT 270
 QY 240 FGGGTKEIK 249
 Db 271 FGGGTKEIK 280

RESULT 10
 AAU72865
 ID AAU72865 standard; protein; 258 AA.
 XX
 AC AAU72865;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE P5-2 single chain Fv.
 XX
 KW Human; NK2D; NK2D receptor complex; cancer; infectious disease; tumour;
 KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
 KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
 KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
 KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DA10;
 KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
 KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
 KW P4-15; P5-2; P5-3; P5-9; P5-11; P5-12; 3B10xP4-3; 3B10xP4-14;
 KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
 XX
 OS Homo sapiens.
 XX
 PN WC200171005-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 26-MAR-2001; 2001WO-EP003414.
 XX
 PR 24-MAR-2000; 2000EP-00106467.
 XX
 PA (KUFE/) KUFER P.
 PI Kufner P, Riettmueller G, Lutterbuese R, Borschert K, Kischel R;
 PI Mayer M, Hofmeister R;
 DR WPI; 2002-055119/07.
 DR N-PSDB; AAS97139.
 XX

Multifunctional polypeptides comprising binding sites that specifically recognize extracellular groups of the NK2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and infectious diseases.

Example 7; Fig 16; 11app; English.

The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NK2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated polynucleotide are used for the preparation of a pharmaceutical composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protozoa or helminths. The autoimmune diseases include multiple sclerosis, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NK2D receptor and the polypeptides of the invention

Sequence 258 AA;
 Query Match 70.8%; Score 931; DB 5; Length 258;

Best Local Similarity 72.5%; Pred. No. 1e-59;
 Matches 179; Conservative 22; Mismatches 40; Indels 6; Gaps 2;

QY 4 LQESGAELVRSQAVNISCTASGNIKDYMHWKORPEGLIEMTIDPESGETEYAPN 63
 Db 5 LEQSGAELMKPGASVKISCKATGYTFSSYIEWWKORPGHGLEMTIDPESGSSTNNYK 64
 QY 64 FQKATVTADTSMTAYLHLSLTSEPTTYYCAVITYEYEDGALDYPWGQGTYYVSSG 123
 Db 65 FKGATVFTADTSMTAYWQSLTSESAVYVCARGLRWF----AWGQGTYYVSSG 119
 QY 124 GGSGGGGGGSDIELTGSSSLAVSAGEKVMSCSSQSLEFSTRKXYLAAYQXP 183
 Db 120 GGSGGGGGGGSELVMTGSPSSILTYAGKVMSCSSQSLSNAGKXLYLTYQXP 179
 QY 184 GQSPKVLITYASTRESGVDPFRFTGSGGTDFTLTITSSVQAEADLAIVYCKQSYNP-TPGG 242
 Db 180 GQPKLITYASTRESGVDPFRFTGSGGTDFTLTITSSVQAEADLAIVYCKQNDYSYDLTFGA 239
 QY 243 GTKLEIK 249
 Db 240 GTKLEIK 246

RESULT 11
 AA17960
 ID AA17960 standard; protein; 248 AA.
 XX
 AC AA17960;
 XX
 DT 04-AUG-1999 (first entry)
 XX
 DE Mouse scFv fragment 4-1.
 XX
 KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
 KW autoimmune disease; scFv-antibody; single-chain Fv; mouse.
 XX
 OS Mus sp.
 XX
 PN W09925818-A1.
 XX
 PD 27-MAY-1999.
 XX
 PF 16-NOV-1998; 98WO-EP007313.
 XX
 PR 17-NOV-1997; 97EP-00120096.
 XX
 PA (KUFE/) KUFER P.
 PI Kufner P, Raum T, Borschert K, Zettl F, Lutterbuese R;
 PI WPI; 1999-338004/28.
 DR N-PSDB; AAX77243.
 XX

Phage display system for identification of binding site domains retaining capacity to bind an epitope.

Claim 27; Fig 6.6; 152pp; English.

The invention relates to a method of identifying binding site domains (BSD) that retain the capacity of binding to a predetermined epitope when positioned C-terminal of at least one further domain in a recombinant bi- or multivalent polypeptide. The method comprises (a) testing a panel of BSD displayed on the surface of a biological display system as part of a fusion protein for binding to a predetermined epitope, where the fusion protein comprises an additional domain positioned N-terminal of the BSD and an amino acid sequence that mediates anchoring of the fusion protein to the surface of the display system; and (b) identifying a BSD that binds to the predetermined epitope. The method is useful to identify bi- or multivalent polypeptides that comprise antibody binding sites capable of efficiently binding to the corresponding antigen. The polypeptides or antibodies identified by the method are useful therapeutically and diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody

fragments that bind independently of their position within bifunctional single-chain fusion proteins can be isolated from combinatorial antibody libraries using the new in vitro method. Sequences AAY1757-965 represent mouse scFv fragments

Sequence 248 AA;
Query Match 70.7%; Score 930; DB 2; Length 248;
Best Local Similarity 72.9%; Pred. No. 1.2e-59;
Matches 180; Conservative 25; Mismatches 38; Indels 4; Gaps 2;

```

QY 4 LOESGAEIVRSASVNLCTASGFNIKDYMHMWKQPEEGLEWIGYIDPESGETEYAPN 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 LEQSAELVREPTSKISKASGYAFITWYQWQRGHGLFWGDLFPESGNHNYEK 64
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 FQKATVTADTSNTAVYHLSLTSEDITVYVCNAVYYEYDGVADYWGQGTIVYSSG 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 FKGKATLTADKSSYTAWYQLSLTSEDGAVYFCALRWMD--EAMDYWGQGTIVYSSG 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 124 GGGSGGGSGGGSGSDIELTQSPSLAVSAGEKVMSCSSQSLFNSRIRKNTLAWYQOKP 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 GGGSGGGSGGGSGSELVMTQSPSLVSAEKVTVSCSSQSLNSGMQKNYLAWYQOKP 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 184 GQSPKVLITWASTRESGVDPDRFTSGSGTDFTLTITSSVQAEDLAVYCKOSYNLP-TEGG 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 GQPKLLITWASTRESGVDPDRFTSGSGTDFTLTITSSVQAEDLAVYCKQNDYSPYTFGG 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 243 GTKLEIK 249
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 242 GTKLEIK 248
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 12

ABJ26742 ID ABJ26742 standard; protein; 240 AA.

XX ABJ26742;

AC 01-MAY-2003 (first entry)

DE VEGF binding related protein SEQ ID No 51.

XX Cytostatic; antibody; antigen binding site; VEGF receptor; mitogenesis;

KM leukaemia cell; vascular endothelial growth factor; tumour;

KM bispecific antigen-binding protein; mouse; murine.

OS Mus sp.

PN WO2003002144-A1.

XX 09-JAN-2003.

PF 26-JUN-2002; 2002WO-US020332.

PR 26-JUN-2001; 2001US-0301299P.

XX (IMCL-) IMCLONE SYSTEMS INC.

PI Zhu Z;

DR WPI; 2003-201468/19.

DR N-PSDB; ABT23322.

PT New bispecific antibodies having antigen-binding sites specific for a first vascular endothelial growth factor (VEGF) receptor and for a second VEGF receptor, useful for inhibiting migration of leukemia cells, or for treating tumors.

PS Disclosure; Page 63; 98pp; English.

XX The invention relates to a novel antibody having a first antigen binding site specific for a first vascular endothelial growth factor (VEGF)

CC receptor and a second antigen-binding site specific for a second VEGF

CC receptor. The bispecific antigen-binding proteins block activation of the VEGF receptor and are useful for reducing or inhibiting VEGF-induced cellular functions such as mitogenesis of vascular endothelial cells and migration of leukaemia cells. The antibodies are useful for treating tumours and for in vivo or in vitro for investigative and diagnostic methods. This sequence represents a mouse protein relating to the bispecific antibodies that bind to the VEGF receptors of the invention

Sequence 240 AA;
Query Match 70.3%; Score 924.5; DB 6; Length 240;
Best Local Similarity 71.2%; Pred. No. 2.8e-59;
Matches 178; Conservative 27; Mismatches 32; Indels 13; Gaps 3;

```

QY 1 QVKLOESGAEIVRSASVNLCTASGFNIKDYMHMWKQPEEGLEWIGYIDPESGETEY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVKLOESGAEIVRSASVNLCTASGFNIKDYMHMWKQPEEGLEWIGYIDPESGETEY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 APNFGKATVTADTSNTAVYHLSLTSEDITVYVCNAVYYEYDGVADYWGQGTIVY 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 DPKQKATLTADTSNTAVYHLSLTSEDITVYVCNAVYYCALPPEY-----FDYWGHTVTV 114
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 SSGSGSGSGGGSGSDIELTQSPSLAVSAGEKVMSCSSQSLFNSRIRKNTLAWYQ 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 115 SSGSGSGSGGGSGSDIELTQSPKFMSTVGVQVSTCKASQVQVDTN-----VAWYQ 168
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 QKPGQSPKVLITWASTRESGVDPDRFTSGSGTDFTLTITSSVQAEDLAVYCKOSYNLP-T 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 169 QKPGQSPKALITWASTRESGVDPDRFTSGSGTDFTLTITSSVQAEDLAVYCKQVNSPYFT 228
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 FGGGTLEIK 249
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 229 FGGGTLEIK 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 13

AAB31422 ID AAB31422 standard; protein; 242 AA.

XX AAB31422;

AC 20-APR-2001 (first entry)

DE Protein used for immunising against shed antigen-specific B cells.

XX Vaccine; shed antigen-specific B cell; idiotypic antibody;

KM immune complex-mediated disease; autoimmune disease;

KM humoral immune response; cancer.

OS Synthetic.

PN WO200076319-A1.

XX 21-DEC-2000.

PF 16-JUN-2000; 2000WO-US016677.

PR 16-JUN-1999; 99US-0139521P.

XX 15-JUN-2000; 2000US-00594985.

PA (BIOC-) BIOCRYSTAL LTD.

PI Nelson MB, Barbera-Guillem E;

DR WPI; 2001-080635/09.

PT Inducing an immune response against shed antigen-specific B cell idiotypes, by administering a vaccine formulation comprising polynucleotides encoding an idiotypic determinant or peptides comprising an idiotypic determinant.

XX Example 2; Page 66-67; 81pp; English.

CC The present sequence represents a synthetic protein which may be used in
 CC vaccines for inducing immune responses of the invention. The protein
 CC comprises a VH region linked to a VL region. The specification describes
 CC a method for inducing an immune response reactive with idiotypes present
 CC on shed antigen-specific B cells (SAB) of an individual. The method
 CC involves administering a vaccine formulation comprising polynucleotide
 CC encoding an idiotype of an antibody that binds to an epitope of shed
 CC antigen. The method is useful for inducing an immune response reactive
 CC with idiotypes present on SAB of an individual. The method is useful for
 CC depleting shed antigen-specific B cells, and for treating immune complex-
 CC mediated disease progression in organ specific autoimmune disease
 CC exacerbated by humoral immune response against groups expressed on shed
 CC antigen, or by plasma cell production of antibodies against groups of
 CC shed antigen. It is useful in cancer therapy and for treating autoimmune
 CC disease
 CC
 SQ Sequence 242 AA;

Query Match 70.2%; Score 923.5; DB 4; Length 242;
 Best Local Similarity 70.0%; Pred. No. 3.4e-59;
 Matches 175; Conservative 29; Mismatches 37; Indels 9; Gaps 2;

QY 1 QVQLQESGAEIVRSASVNLSTASGFNIKDYVMHWKORPEGLIEWIGYIDPSSETEY 60
 Db 1 QVQLQESGAEIVRSASVNLSTASGFNIKDYVMHWKORPEGLIEWIGYIDPSSETEY 60
 QY 61 AEPNQGKATVTADTSSNTAYLHLSTLSEDTVTYYCNNAVYYEDYALDYWGQGTVTYV 120
 Db 61 NEKFKGKATLTADKSSSTAYVQNLSTSEDSAVYFCRSYY-----GHMGGTITVTV 112
 QY 121 SSGGGSGGGSGGGSGGSDIELTQSPSSLAVSAGEKYAMSCSSQSLFNSRTRKNYLAWYQ 180
 Db 113 SSGGGSGGGSGGGSGGSDIYWSQSPSSLPVSGEKVTLSCSSQSLILYSGNKNYLAWYQ 172
 QY 181 QKPGQSPKVLIIYASTRESGVPPRFTGSGSDTFTLTISVQAEDLAAYYCKQSYNLP-T 239
 Db 173 QKPGQSPKVLIIYASTRESGVPPRFTGSGSDTFTLTISVKTEDLAAYYCKQSYNLP-T 232
 QY 240 FGGGTKEIK 249
 Db 233 FGGGTKEIK 242

RESULT 14
 ID AAY17964 standard; protein; 248 AA.

AC AAY17964;
 DT 04-AUG-1999 (first entry)
 DE Mouse scFv fragment 5-10.
 KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
 KW autoimmune disease; scFv-antibody; single-chain Fv; mouse.
 OS Mus sp.
 PN WO9925818-A1.
 PD 27-MAY-1999.
 PF 16-NOV-1998; 98WO-BP007313.
 PR 17-NOV-1997; 97EP-00120096.
 PA (KUFER/) KUFER P.
 PI Kufner P, Raum T, Borschert K, Zetl F, Lutterbuese R;
 DR WPI, 1999-338004/28.
 DR N-PSDB; AAX77247.
 XX

PT Phage display system for identification of binding site domains retaining
 PT capacity to bind an epitope.

PS Claim 27, Fig 6.10; 152pp; English.

CC The invention relates to a method of identifying binding site domains
 CC (BSD) that retain the capacity of binding to a predetermined epitope when
 CC positioned C-terminal of at least one further domain in a recombinant bi-
 CC or multivalent polypeptide. The method comprises (a) testing a panel of
 CC BSD displayed on the surface of a biological display system as part of a
 CC fusion protein for binding to a predetermined epitope, where the fusion
 CC protein comprises an additional domain positioned N-terminal of the BSD
 CC and an amino acid sequence that mediates anchoring of the fusion protein
 CC to the surface of the display system; and (b) identifying a BSD that
 CC binds to the predetermined epitope. The method is useful to identify bi-
 CC or multivalent polypeptides that comprise antibody binding sites capable
 CC of efficiently binding to the corresponding antigen. The polypeptides or
 CC antibodies identified by the method are useful therapeutically and
 CC diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
 CC fragments that bind independently of their position within bifunctional
 CC single-chain fusion proteins can be isolated from combinatorial antibody
 CC libraries using the new in vitro method. Sequences AAY1957-965 represent
 CC mouse scFv fragments
 CC
 SQ Sequence 248 AA;

Query Match 70.0%; Score 921; DB 2; Length 248;
 Best Local Similarity 71.7%; Pred. No. 5.2e-59;
 Matches 177; Conservative 25; Mismatches 41; Indels 4; Gaps 2;

QY 4 IQESGAEIVRSASVNLSTASGFNIKDYVMHWKORPEGLIEWIGYIDPSSETEYAPN 63
 Db 5 IQESGAEIVRSASVNLSTASGFNIKDYVMHWKORPEGLIEWIGYIDPSSETEYAPN 64
 QY 64 FQKATVTADTSSNTAYLHLSTLSEDTVTYYCNNAVYYEDYALDYWGQGTVTYVSSG 123
 Db 65 FQKATLTADKSSSTAYVQNLSTSEDSAVYFCRSYY-----EPMDYMGQGTITVTVSSG 121
 QY 124 GGGSGGGSGGGSGGSDIELTQSPSSLAVSAGEKYAMSCSSQSLFNSRTRKNYLAWYQOKP 183
 Db 122 GGGSGGGSGGGSGGSDIYWSQSPSSLVTITAGEKYAMSCSSQSLILYSGNKNYLAWYQOKP 181
 QY 184 GQSPKVLIIYASTRESGVPPRFTGSGSDTFTLTISVQAEDLAAYYCKQSYNLP-TFGG 242
 Db 182 GQPPKVLIIYASTRESGVPPRFTGSGSDTFTLTISVQAEDLAAYYCKQSYNLP-TFGA 241
 QY 243 GTKLEIK 249
 Db 242 GTKLEIK 248

RESULT 15
 ID AAE25963 standard; protein; 238 AA.

AC AAE25963;
 DT 15-NOV-2002 (first entry)
 DE KDR binding immunoglobulin related mouse protein #3.
 KW Mouse; immunoglobulin; kinase insert domain-containing receptor; KDR;
 KW foetal liver kinase; FLK-1 receptor; vascular endothelial growth factor;
 KW VEGF; tumour growth; heavy chain variable region; VH; angiogenesis;
 KW pIC11; scFv antibody.
 OS Mus sp.
 PN US2002064528-A1.
 PD 30-MAY-2002.
 DR 12-OCT-2001; 2001US-00976787.
 PF

XX 28-JAN-2000; 2000US-00493539.
 PR (ZHUZ/) ZHU Z.
 XX (WITT/) WITTE U.
 PA
 XX Zhu Z, Witte U;
 PI
 XX WPI; 2002-589175/63.
 DR
 XX Novel immunoglobulin molecule for reducing tumor growth, binds to kinase
 PT insert domain-containing receptor with an affinity comparable to human
 PT vascular endothelial growth factor, and neutralizes activation of KDR.
 XX
 PS Disclosure; Page 17-18; 34pp; English.
 XX
 CC The present invention relates to novel immunoglobulin molecules that bind
 CC to kinase insert domain-containing receptor (KDR) (a human homologue of
 CC mouse foetal liver kinase (FLK)-1 receptor) with an affinity comparable
 CC to human vascular endothelial growth factor (VEGF) and that neutralises
 CC activation of KDR. Sequences of the invention are useful for neutralising
 CC the activation of KDR, for reducing tumour growth and for inhibiting
 CC angiogenesis. The present sequence is KDR binding immunoglobulin related
 CC mouse protein
 CC
 SQ Sequence 238 AA;

Query Match 69.8%; Score 917.5; DB 5; Length 238;
 Best Local Similarity 70.4%; Pred. No. 9e-59;
 Matches 176; Conservative 30; Mismatches 31; Indels 13; Gaps 4;

QY 1 QVKLQESGAEIVRSAGASVNLSTASGPNIKDYMHVWKQRPBEGLEWIGYIDPSGETEY 60
 Db 1 QVKLQSGAGAEIVRSAGASVNLSTASGPNIKDYMHVWKQRPBEGLEWIGWIDPENGSDY 60
 QY 61 APNFQGAITYTADTSSNTAYIHLSLTSEDTTYVCNAVITYEYDGYALDYWGQGTIVTV 120
 Db 61 APNFQGAITYTADTSSNTAYIHLSLTSEDTTYVCNAVITYEYDGYALDYWGQGTIVTV 115
 QY 121 SSGGGSGGGGGGGGGSDIELTQSPSSILAVSAGEKVMSCSKSOSLFPNSRTRKNYLAHQ 180
 Db 116 SSGGGSGGGGGGGGGSDIELTQSPALMSASPGKVTITCSASSV-----SYMHWFQ 168
 QY 181 QKPGQSPKVLITYMASTRSGVDPDRFTGSGGTDFTLTISVQAPDLAVYCKQSYNLP-T 239
 Db 169 QKPGSPKVLITYSTSNLASGVPARFSGSGSTSYLTISRMEDADATYYCQRRSSYPFT 228
 QY 240 FGGGTKLEIK 249
 Db 229 FGGGTKLEIK 238

Search completed: July 30, 2004, 11:19:21
 Job time : 50.0915 secs

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OM protein - protein search, using sw model

Run on: July 30, 2004, 11:17:36 ; Search time 14.6768 Seconds
(without alignments)
875.861 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1315

Sequence: 1 QVKLQSGAEIVRSASVNL.....YCKQSYNLPFGGKLEIK 249

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/PCOMUS_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1024.5	77.9	288	4	US-09-423-439-38
2	1024.5	77.9	673	4	US-09-423-439-32
3	955	72.6	535	4	US-08-983-035A-38
4	906	68.9	281	4	US-09-423-439-44
5	883	67.1	270	2	US-08-652-507-2
6	877.5	66.7	282	2	US-08-860-174A-10
7	877	66.7	553	2	US-08-661-052-16
8	877	66.7	553	3	US-09-188-082-16
9	877	66.7	553	4	US-09-364-088-16
10	877	66.7	553	4	US-10-102-716-16
11	877	66.7	553	4	US-10-092-246-36
12	854	64.9	240	4	US-10-092-246-35
13	846	64.3	248	4	US-09-649-063-23
14	842.5	64.1	249	2	US-09-984-186-18
15	842.5	64.1	249	4	US-09-984-186-18
16	839	63.8	240	4	US-10-092-246-37
17	837	63.7	240	4	US-10-092-246-35
18	831.5	63.2	277	2	US-08-256-790-2
19	830	63.1	269	3	US-08-646-265A-109
20	823.5	62.6	244	2	US-08-553-497A-20
21	818	62.2	301	3	US-08-661-052-14
22	818	62.2	301	3	US-09-188-082-14
23	818	62.2	301	4	US-09-364-088-14
24	818	62.2	301	4	US-09-102-716-14
25	813.5	61.9	242	2	US-08-553-497A-26
26	811.5	61.7	246	2	US-08-553-497A-24
27	808.5	61.5	244	2	US-08-553-497A-22

28	807.5	61.4	482	4	US-09-509-031-16	Sequence 16, Appl
29	803.5	61.1	483	2	US-08-392-338A-19	Sequence 19, Appl
30	803.5	61.1	483	3	US-09-166-750-19	Sequence 19, Appl
31	803.5	61.1	483	3	US-09-166-093-19	Sequence 19, Appl
32	803.5	61.1	483	3	US-09-172-019-19	Sequence 19, Appl
33	803.5	61.1	483	3	US-09-166-094-19	Sequence 19, Appl
34	803.5	61.1	483	4	US-09-443-213-19	Sequence 19, Appl
35	800.5	60.9	242	2	US-08-553-497A-28	Sequence 28, Appl
36	799	60.8	240	4	US-10-092-246-34	Sequence 34, Appl
37	799	60.8	265	2	US-08-403-853-16	Sequence 16, Appl
38	798.5	60.7	239	4	US-10-092-246-33	Sequence 33, Appl
39	797	60.6	256	4	US-09-526-738A-2	Sequence 2, Appl
40	797	60.6	258	4	US-09-526-738A-4	Sequence 4, Appl
41	796	60.5	273	2	US-08-403-853-18	Sequence 18, Appl
42	795.5	60.5	244	4	US-09-244-369B-1	Sequence 1, Appl
43	794	60.4	348	4	US-09-646-028-12	Sequence 12, Appl
44	794	60.4	361	4	US-09-646-028-14	Sequence 14, Appl
45	790	60.1	297	4	US-09-486-814A-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6338070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-NOV-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 288 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-423-439-38

Query Match 77.9%, Score 1024.5, DB 4, Length 288;
Best Local Similarity 77.9%, Pred. No. 4.4e-78;
Matches 194, Conservative 21, Mismatches 33, Indels 1, Gaps 1;

QY 1 QVKLQSGAEIVRSASVNLCTASGFKIRYMAWVQRPBEGLEWIGYIDPESGRTY 60
DB 23 QVQKQGPAAELVFKGASVYOLSCKASGYFTGTWYHWPQKQGLEWIGVNPSTGRSDY 82
QY 61 APNFQKATVADSSNTAYLHLSTLSEDTVYVCNAVITYEYDGYALDPWGQGTWTV 120
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Db 83 NEKFNKATLTVDKSSTTAYWQLSLTSEDSAVVYCARERAYGDD-ANDYWGQGTIVTV 141
QY 121 SSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVMSCKSQSLFNSRTRKNYLAAYQ 180
Db 142 SSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVMSCKSQSLFNSRTRKNYLAAYQ 201
QY 181 QRPQGSFKVLIYMASTRSGVDPDRFTSGSGSDTFTLTSSVQAEADLAIVYCKQSYLPTF 240
Db 202 QRPQGSFKVLIYMASTRSGVDPDRFTSGSGSDTFTLTSSVQAEADLAIVYCKQSYLPTF 261
QY 241 GGGTKLEIK 249
Db 262 GGGTKLEIK 270

RESULT 2
US-09-423-439-32

/ Sequence 32, Application US/09423439
/ Patent No. 6339070
/ GENERAL INFORMATION:
/ APPLICANT: EMERY, Stephen Charles
/ BLAKEY, David Charles
/ TITLE OF INVENTION: CHEMICAL COMPOUNDS
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pillsbury Winthrop, L.L.P.
/ STREET: 1100 New York Ave., N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: MS Word
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/423,439
/ FILING DATE: 09-NO. 6339070-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/GB98/01294
/ FILING DATE: 05-MAY-1998
/ APPLICATION NUMBER: GB 9709421.3
/ FILING DATE: 10-MAY-1997
/ INFORMATION FOR SEQ ID NO: 32:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 673 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-423-439-32

Query Match 77.9%; Score 1024.5; DB 4; Length 673;
Best Local Similarity 77.9%; Pred. No. 1.2e-77;
Matches 194; Conservative 21; Mismatches 33; Indels 1; Gaps 1;
QY 1 QVKLOESGAEIVRSGASVNLSTASGFNIKDYMHMWKQRPBEGLEWIGYIDPSSGETEY 60
Db 20 QVQLDQPGAEIVKPKASVQLSCKASGYFTGWIHWKQRPQGLGIEWIGENVPSTGRSDY 79
QY 61 APNFOGKATVADTSSNTAYVHLSSLTSEDTTVYYCNAVITYEYDVALDYWGQGTIVTV 120
Db 80 NEKFNKATLTVDKSSTTAYWQLSLTSEDSAVVYCARERAYGDD-ANDYWGQGTIVTV 138
QY 121 SSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVMSCKSQSLFNSRTRKNYLAAYQ 180
Db 139 SSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVMSCKSQSLFNSRTRKNYLAAYQ 198
QY 181 QRPQGSFKVLIYMASTRSGVDPDRFTSGSGSDTFTLTSSVQAEADLAIVYCKQSYLPTF 240

Db 199 QRPQGSFKVLIYMASTRSGVDPDRFTSGSGSDTFTLTSSVQAEADLAIVYCKQSYLPTF 258
QY 241 GGGTKLEIK 249
Db 259 GGGTKLEIK 267

RESULT 3
US-08-983-035A-38

/ Sequence 38, Application US/08983035A
/ Patent No. 6326464
/ GENERAL INFORMATION:
/ APPLICANT: CONSEILLER, EMMANUEL
/ BRACCO, LAURENT
/ TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
/ USES THEREOF
/ NUMBER OF SEQUENCES: 59
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
/ DUNNER, LLP
/ STREET: 1300 I Street, NW
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20005-3315
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/983,035A
/ FILING DATE: 20-Feb-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/FR96/01111
/ FILING DATE: 17-JUL-1996
/ APPLICATION NUMBER: FR 95/08729
/ FILING DATE: 19-JUL-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Strauss, William L.
/ REGISTRATION NUMBER: 47,114
/ REFERENCE/DOCKET NUMBER: 03804.0142
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 38:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 535 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-08-983-035A-38

Query Match 72.6%; Score 955; DB 4; Length 535;
Best Local Similarity 74.4%; Pred. No. 6.1e-72;
Matches 186; Conservative 23; Mismatches 33; Indels 8; Gaps 3;
QY 1 QVKLOESGAEIVRSGASVNLSTASGFNIKDYMHMWKQRPBEGLEWIGYIDPSSGETEY 60
Db 3 QVQLDQPGAEIVKPKASVQLSCKASGYFTGWIHWKQRPQGLGIEWIGENVPSTGRSDY 62
QY 61 APNFOGKATVADTSSNTAYVHLSSLTSEDTTVYYCNAVITYEYDVALDYWGQGTIVTV 120
Db 63 APKQOGKATVADTSSNTAYVQLSLASSEDIAVYYCN-----PYGALDYWGQGTIVTV 116
QY 121 SSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVMSCKSQSLFNSRTRKNYLAAYQ 180
Db 117 SSGGGSGGGSGGGSDVLTQSPSSLAVSAGEKVMSCKSQSLFNSRTRKNYLAAYQ 175
QY 181 QRPQGSFKVLIYMASTRSGVDPDRFTSGSGSDTFTLTSSVQAEADLAIVYCKQSYLPTF 239

D _b	176	QRPGQSKRLIIVYSKLDGSDPDRFTGSGSDFTLKINRVAEDLGYVCWQGTHTSPLT	235
Q _Y	240	FGGRTKLEIK	249
		:	
D _b	236	FGAGTKLELK	245

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1      RESULT 4
2      US-09-423-439-44
3      ; Sequence 44, Application US/09423439
4      ; Patent No. 6339070
5      ;
6      GENERAL INFORMATION:
7      APPLICANT: EMERY, Stephen Charles
8      BLAKEY, David Charles
9      ;
10     TITLE OF INVENTION: CHEMICAL COMPOUNDS
11     ;
12     NUMBER OF SEQUENCES: 60
13     ;
14     CORRESPONDENCE ADDRESS:
15     ADDRESSEE: Pillsbury Winthrop, L.L.P.
16     STREET: 1100 New York Ave., N.W.
17     CITY: Washington
18     STATE: D.C.
19     COUNTRY: U.S.A.
20     ZIP: 20005
21     ;
22     COMPUTER READABLE FORM:
23     MEDIUM TYPE: Floppy disk
24     ;
25     COMPUTER: IBM PC compatible
26     ;
27     OPERATING SYSTEM: PC-DOS/MS-DOS
28     SOFTWARE: MS word
29     ;
30     CURRENT APPLICATION DATA:
31     APPLICATION NUMBER: US/09/423,439
32     FILING DATE: 09-No. 6339070-1999
33     CLASSIFICATION: <Unknown>
34     ;
35     PRIOR APPLICATION DATA:
36     APPLICATION NUMBER: PCT/GB98/01294
37     FILING DATE: 05-MAY-1998
38     APPLICATION NUMBER: GB 9709421.3
39     FILING DATE: 10-MAY-1997
40     ;
41     INFORMATION FOR SEQ ID NO: 44:
42     SEQUENCE CHARACTERISTICS:
43     LENGTH: 281 amino acids
44     TYPE: amino acid
45     STRANDEDNESS: single
46     TOPOLOGY: linear
47     ;
48     MOLECULE TYPE: protein
49     ;
50     SEQUENCE DESCRIPTION: SEQ ID NO: 44:
51     US-09-423-439--44

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Db      194  QKGTSLKMLTYSISNLASGVPA+RFSSGSGTSTSLTISRMEADAA+TYCQQRSTYELT 253
QY      240  FGGGT+KDELK 249
Db      254  FGAGTKLEIK 263

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```

US-09-423-439-51
; Sequence 51, Application US/09423439
; Patent No. 6339070
;
; GENERAL INFORMATION:
;
; APPLICANT: EMERY, Stephen Charles
;           BLAKEY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS word
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/09/423,439
; FILING DATE: 09-NO. 6339070-1999
;
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: PCT/GB98/01294
; FILING DATE: 05-MAY-1998
; APPLICATION NUMBER: GB 9709421.3
; FILING DATE: 10-MAY-1997
;
; INFORMATION FOR SEQ ID NO: 51:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 666 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-423-439-51

```

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RESULT 6
US-08-652-507-2
; Sequence 2, Application US/08652507
; Patent No. 5876691
;
GENERAL INFORMATION:
;
APPLICANT:
;
TITLE OF INVENTION: ANTIBODY AGAINST CARCINOEMBRYONIC ANTIGEN
;
TITLE OF INVENTION:
;
NUMBER OF SEQUENCES: 8

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderyhe, P.C.
STREET: 1100 No. 5876691th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,507
FILING DATE: 02-Jul-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 117-211
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-507-2

Query Match 67.1%; Score 883; DB 2; Length 270;
Best Local Similarity 67.1%; Pred. No. 2,7e-66;
Matches 171; Conservative 28; Mismatches 36; Indels 20; Gaps 4;

QY 1 QVQLQESGAEIVRSASVNICTASGPNIKDYVMHWKORPEBEGLEWIGYIDPSGTEY 60
DB 27 QVQLQESGAEIVRSASVNICTASGPNIKDYVMHWKORPEBEGLEWIGYIDPSGTEY 86
QY 61 APNQGKATVTADSSNTAYLHLSLTSEDTVYVCNAVIYYEDG-----YALDYWGQG 115
DB 87 APNQGKATVTADSSNTAYLHLSLTSEDTVYVCNAVIYYEDG-----YALDYWGQG 139
QY 116 TTVVSSGGGGSGGGSGGGSDIELTQSPSSLAVSAGEKYAMCKSSQSLFNSRTKKNY 175
DB 140 TTVVSSGGGGSGGGSGGGSENVLITQSPALMGASPGKEKVTITCSASSV-----SY 192
QY 176 LAWYQKRGQSPKLIYVASTRESGVPRFTGSGSGTDFLTITSSVOAEDLAVYCKQSY 235
DB 193 MEMFOQKRGTSPKLMTYSTSLMAGVPRFSGSGSGLSYLTISRMEDLAATYYCQQR 252
QY 236 NLPTFGAGTKLEIK 249
DB 253 SYPLTFGAGTKLEIK 267

RESULT 7

US-08-860-174A-10
Sequence 10, Application US/08860174A
Patent No. 5989830
GENERAL INFORMATION:
APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOGT, Cornelis Paul Erik
APPLICANT: VERHOEIJEN, Martine Elisa
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
STREET: 9th Floor, East Tower
CITY: WASHINGTON, D.C.

STATE: UNITED STATES
COUNTRY: 3918
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,174A
FILING DATE: June 16, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95307332.7
FILING DATE: October 16, 1995
APPLICATION NUMBER: PCT/EP/96/03605
FILING DATE: August 14, 1996
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-860-174A-10

Query Match 66.7%; Score 877.5; DB 2; Length 282;
Best Local Similarity 68.0%; Pred. No. 8.3e-66;
Matches 170; Conservative 20; Mismatches 57; Indels 3; Gaps 3;

QY 1 QVQLQESGAEIVRSASVNICTASGPNIKDYVMHWKORPEBEGLEWIGYIDPSGTEY 60
DB 23 QVQLQESGAEIVRSASVNICTASGPNIKDYVMHWKORPEBEGLEWIGYIDPSGTEY 82
QY 61 APNQGKATVTADSSNTAYLHLSLTSEDTVYVCNAVIYYEDG-----YALDYWGQG 120
DB 83 SDNVKGFRTSRDNGKNTLYLQMSLSKSEDTAYYCARHGYG-KGY-FYWGQGLTVV 140
QY 121 SSGGGSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKYAMCKSSQSLFNSRTKKNY 180
DB 141 SSGGGSGGGSGGGSGGGSDIELTQSPSSLAVSAGEKYAMCKSSQSLFNSRTKKNY 200
QY 181 QKPGQSPKLIYVASTRESGVPRFTGSGSGTDFLTITSSVOAEDLAVYCKQSY 239
DB 201 QKPGQSPKLIYVASTRESGVPRFTGSGSGTDFLTITSSVOAEDLAVYCKQSY 260
QY 240 FGGGSKLEIK 249
DB 261 FGGGSKLEIK 270

RESULT 8

US-08-661-052-16
Sequence 16, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezia Somanadaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

RESULT 10
 US-09-364-088-16
 Sequence 16, Application US/09364088
 Patent No. 6365161
 GENERAL INFORMATION:
 APPLICANT: Yashwant M. Deo, et al.
 TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
 TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD, LLP
 STREET: 28 State Street, 24th Floor
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/364,088
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/188,082
 FILING DATE: 07-JUNE-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/484,172
 FILING DATE: 07-JUNE-1995

ATTORNEY/AGENT INFORMATION:

NAME: Remillard, Jane E.

REGISTRATION NUMBER: 38, 872

REFERENCE/DOCKET NUMBER: MXI-043CP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)742-7414

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-364-088-16

Query Match

Best Local Similarity 66.5%; Pred. No. 2,1e-65;

Matches 169; Conservative 29; Mismatches 36; Indels 20; Gaps 4;

Query

Db

2 VKLOESGAEIVRSASVNLCTASGFNPKDYMHVWKQPREGLWIGYIDPESGETEYA 61

278 IKLOESGAEIVRSASVNLCTASGFNPKDYMHVWKQPREGLWIGYIDPESGETEYA 337

62 PNFQKATVLTADTSNTAYLHLSTSEDTVYVCNAVITYEYDG-----YALDYWGQGT 116

338 PKFQKATFTDTSSNTAYLQLSLTSEDTAVYCN-----BETPGPYFFDYWGQGT 390

117 TVTVSSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYL 176

391 TVTVSSGGGSGGGSGGGSENVLTOGPAIMASAPGKVTITCSASSV-----SYM 443

177 AMYQKPGQSPKVLTYMASTRSGVPDRFTSGSGGTDEFTLTSSVQADLAIVYCKQSYN 236

444 HMFQKPGTSPKLTYSNTSLASGVPAFSGSGGTSLTISRMEADDAITYCQQRSS 503

Db

237 LP-TPGGTKLEIK 249

504 YPLTFGAGTKLEIK 517

Db

237 LP-TPGGTKLEIK 249

504 YPLTFGAGTKLEIK 517

Db

237 LP-TPGGTKLEIK 249

504 YPLTFGAGTKLEIK 517

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237 LP-TPGGTKLEIK 249

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504 YPLTFGAGTKLEIK 517

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237 LP-TPGGTKLEIK 249

504 YPLTFGAGTKLEIK 517

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237 LP-TPGGTKLEIK 249

504 YPLTFGAGTKLEIK 517

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237 LP-TPGGTKLEIK 249

504 YPLTFGAGTKLEIK 517

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237 LP-TPGGTKLEIK 249

504 YPLTFGAGTKLEIK 517

Db

237 LP-TPGGTKLEIK 249

504 YPLTFGAGTKLEIK 517

REFERENCE/DOCKET NUMBER: MXI-043CP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-102-716-16

Query Match

Best Local Similarity 66.5%; Pred. No. 2,1e-65;

Matches 169; Conservative 29; Mismatches 36; Indels 20; Gaps 4;

Query

Db

2 VKLOESGAEIVRSASVNLCTASGFNPKDYMHVWKQPREGLWIGYIDPESGETEYA 61

278 IKLOESGAEIVRSASVNLCTASGFNPKDYMHVWKQPREGLWIGYIDPESGETEYA 337

62 PNFQKATVLTADTSNTAYLHLSTSEDTVYVCNAVITYEYDG-----YALDYWGQGT 116

338 PKFQKATFTDTSSNTAYLQLSLTSEDTAVYCN-----BETPGPYFFDYWGQGT 390

117 TVTVSSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYL 176

391 TVTVSSGGGSGGGSGGGSENVLTOGPAIMASAPGKVTITCSASSV-----SYM 443

177 AMYQKPGQSPKVLTYMASTRSGVPDRFTSGSGGTDEFTLTSSVQADLAIVYCKQSYN 236

444 HMFQKPGTSPKLTYSNTSLASGVPAFSGSGGTSLTISRMEADDAITYCQQRSS 503

Db

237 LP-TPGGTKLEIK 249

504 YPLTFGAGTKLEIK 517

Db

237 LP-TPGGTKLEIK 249

504 YPLTFGAGTKLEIK 517

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237 LP-TPGGTKLEIK 249

504 YPLTFGAGTKLEIK 517

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237 LP-TPGGTKLEIK 249

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237 LP-TPGGTKLEIK 249

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237 LP-TPGGTKLEIK 249

504 YPLTFGAGTKLEIK 517

Db

237 LP-TPGGTKLEIK 249

504 YPLTFGAGTKLEIK 517

Db

237 LP-TPGGTKLEIK 249

REFERENCE/DOCKET NUMBER: MXI-043CP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 553 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-102-716-16

Query Match

Best Local Similarity 64.9%; Score 854; DB 4; Length 240;

Matches 162; Conservative 33; Mismatches 41; Indels 14; Gaps 3;

Query

Db

1 QVKLOESGAEIVRSASVNLCTASGFNPKDYMHVWKQPREGLWIGYIDPESGETEYA 60

3 QVKLOESGAEIVRSASVNLCTASGFNPKDYMHVWKQPREGLWIGYIDPESGETEYA 62

61 APNFOGKATVLTADTSNTAYLHLSTSEDTVYVCNAVITYEYDGAYADYWGQGTTVTV 120

63 SETFKKATLTVDTSNTAYLHLSTSEDTVYVCNAVITYEYDGAYADYWGQGTTVTV 115

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

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121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

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121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

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121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

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121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

121 SSGGGSGGGSGGGSDIELTQSPSSLAIVAGKVMCKSSQSLFNSRTRKNYLAWQ 180

Db

Db 116 SGGGSGGGGGGGSDILTQSPNSLSTIGRIRITCKASODVTA-----VGMVQ 169
QY 181 QKPGSPKVLTYMASTRESGVDPDRFTSGSGSTDEFTLTITSSVQADLAIVYCKOSYNLP-T 239
Db 170 QRPQSPPLTFMSTNHTITVPDRFTSGSGSTDEFTLTITSSVQADLAIVYCKOSYNLP-T 229
QY 240 FGGGTKLEIK 249
Db 230 FGGGTKLEIK 239

RESULT 13

US-09-649-063-23
Sequence 23, Application US/09649063
Patent No. 6600022
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakui
USHO, Shimpel
KUNITAKA, Toshio
KURIMOTO, Masashi
TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/649,063
FILING DATE: 29-Aug-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,140
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 52,526/1997
FILING DATE: 21-FEB-1997
APPLICATION NUMBER: JP 163,490/1997
FILING DATE: 6-JUN-1997
APPLICATION NUMBER: JP 215,490/1997
FILING DATE: 28-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 248
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-649-063-23

Query Match 64.3%; Score 846; DB 4; Length 248;
Best local Similarity 63.6%; Pred. No. 3e-63;
Matches 159; Conservative 37; Mismatches 44; Indels 10; Gaps 3;

QY 1 QVKLQSGAEIVRSGASVNLSTASGENIKDYMHMVKQRPBESLWMTGYIDPESGETEY 60
Db 1 EVQLQSSAEIVRSGASVNLSTASGENIKDYMHMVKQRPBESLWMTGYIDPESGETEY 60
QY 61 APNFGKATVADTSNTAYLHLSTLSEDTTVYVCNAVYYEYDGYALDWGGCTTVTV 120

Db 61 GPNFQDKATITADTSNTAYLQLRLTSEDTTAVYCCRRGNY---GAGFGYWGQGITVTV 117
QY 121 SGGGSGGGGGGGSDILTQSPNSLSTIGRIRITCKASODVTA-----VGMVQ 169
Db 118 SAGGSGGGGGGGSDILTQSPNSLSTIGRIRITCKASODVTA-----VGMVQ 169
QY 181 QKPGSPKVLTYMASTRESGVDPDRFTSGSGSTDEFTLTITSSVQADLAIVYCKOSYNLP-T 239
Db 172 QRPQSPPLTFMSTNHTITVPDRFTSGSGSTDEFTLTITSSVQADLAIVYCKOSYNLP-T 229
QY 240 FGGGTKLEIK 249
Db 232 FGGGTKLEIK 241

RESULT 14

US-08-797-689-18
Sequence 18, Application US/08797689
Patent No. 5876969
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
APPLICANT: Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3043
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 249 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-797-689-18

Query Match 64.1%; Score 842.5; DB 2; Length 249;
Best local Similarity 64.6%; Pred. No. 6e-63;
Matches 164; Conservative 39; Mismatches 38; Indels 13; Gaps 4;

QY 1 QVKLQSGAEIVRSGASVNLSTASGENIKDYMHMVKQRPBESLWMTGYIDPESGETEY 60

```

Db      4 QVQLQSGEELVKKPGASVYKISCKASGYAFSRSMWVVKORPGQGLEWIGRIYFGDGTXY 63
QY      61 APNPGKATVYVADTSNTAYLHLSSLTSDTYVYC---NAVITYEYDVALDYWGQGT 116
Db      64 NGKFKGKATLITADRSSSTAYMQLSLITVGSAYVFCAKENNR--FDERGYAMDYWGQGT 121
QY      117 TTVSSGGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVAMSCKSQGLFNSRTKNTL 176
Db      122 TTVSSGGGGSGGGSGGGSNITLTQSPNSMTSVGDVRSITCKASQDVDTIS-----V 175
QY      177 AMYQKPGQSPKVLITWASTRESGVDPDFTGSGSGTDFLTITSSVQAEPLAVYCKQSYN 236
Db      176 AMYQKPGQSPKVLITWASTRHTGVDPDFTGSGSGTDFLTITSSVQSEDSADYFCQQYSS 235
QY      237 LP-TFGGGTKLEIK 249
Db      236 YPWTFGGGTKLEIK 249

RESULT 15
US-09-984-186-18
; Sequence 18, Application US/09984186
; Patent No. 6686172
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guilton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcoia Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,186
; FILING DATE: 29-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

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US-09-984-186-18
Query Match      64.1%; Score 842.5; DB 4; Length 249;
Best Local Similarity 64.6%; Pred No. 66-63;
Matches 164; Conservative 39; Mismatches 38; Indels 13; Gaps 4;

QY      1 QVQLQSGAEIVRSGASVNLSTASGPNIKDYMHVWVKORPERGLFWIGRIYFGDGTXY 60
Db      4 QVQLQSGEELVKKPGASVYKISCKASGYAFSRSMWVVKORPGQGLEWIGRIYFGDGTXY 63
QY      61 APNPGKATVYVADTSNTAYLHLSSLTSDTYVYC---NAVITYEYDVALDYWGQGT 116
Db      64 NGKFKGKATLITADRSSSTAYMQLSLITVGSAYVFCAKENNR--FDERGYAMDYWGQGT 121
QY      117 TTVSSGGGGSGGGSGGGSDIELTQSPSSLAVSAGEKVAMSCKSQGLFNSRTKNTL 176
Db      122 TTVSSGGGGSGGGSGGGSNITLTQSPNSMTSVGDVRSITCKASQDVDTIS-----V 175
QY      177 AMYQKPGQSPKVLITWASTRESGVDPDFTGSGSGTDFLTITSSVQAEPLAVYCKQSYN 236
Db      176 AMYQKPGQSPKVLITWASTRHTGVDPDFTGSGSGTDFLTITSSVQSEDSADYFCQQYSS 235
QY      237 LP-TFGGGTKLEIK 249
Db      236 YPWTFGGGTKLEIK 249

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Search completed: July 30, 2004, 11:22:27
Job time : 15.6768 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 30, 2004, 11:16:36 ; Search time 13.6646 Seconds
(without alignments)
1752.823 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1315
Sequence: 1 QVTLQSGAEIVRSGASVNL.....YCKQSYNLPFGGTXLEIK 249

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78: *
1: pirl: *
2: pirl2: *
3: pirl3: *
4: pirl4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	857	65.2	268	2 A56446	Ig heavy chain V r
2	854.5	65.0	249	2 S41374	single chain Fv an
3	841.5	64.0	233	2 JCS322	p53 specific singl
4	544	40.9	112	2 S43103	Ig kappa chain V-J
5	538	40.5	113	2 PT0407	Ig light chain V r
6	533	40.5	112	2 PL0265	Ig kappa chain V r
7	533	40.5	133	2 PS0023	Ig kappa chain pre
8	520	39.5	113	2 PT0408	Ig light chain V r
9	514	39.1	112	2 S41393	Ig kappa chain V r
10	503.5	38.3	111	2 S03304	Ig kappa chain V r
11	501.5	38.1	136	2 S04576	Ig heavy chain pre
12	498	37.9	104	2 PH1101	Ig light chain V r
13	497	37.8	103	2 PH1047	Ig light chain V r
14	497	37.8	104	2 PH1102	Ig light chain V r
15	492	37.4	103	2 PH1051	Ig light chain V r
16	492	37.4	103	2 PH1052	Ig light chain V r
17	492	37.4	104	2 PH1104	Ig light chain V r
18	491	37.3	103	2 PH1050	Ig light chain V r
19	489.5	37.2	220	2 A31790	Ig kappa chain V r
20	489	37.2	120	2 G33932	Ig kappa chain pre
21	486	37.0	135	2 S38807	Ig light chain V r
22	486	37.0	178	2 S29594	Ig gamma chain V-J
23	484.5	36.8	113	2 PL0263	Ig kappa chain V r
24	484	36.8	101	2 PH1063	Ig light chain V r
25	484	36.8	104	2 PH1103	Ig light chain V r
26	480	36.5	111	2 G30502	Ig kappa chain V r
27	479	36.4	118	2 PT0356	Ig kappa chain V r
28	478.5	36.4	134	2 PC1214	Ig kappa chain pre
29	477.5	36.3	117	2 S17586	Ig heavy chain V r

30	477.5	36.3	214	2 S69212	Ig kappa chain (Ma
31	475	36.1	138	2 S26040	Ig kappa chain pre
32	474.5	36.1	113	2 PL0264	Ig kappa chain V r
33	474.5	36.1	120	2 S03471	Ig heavy chain V-D
34	470.5	35.8	240	2 S06084	Ig kappa chain pre
35	469	35.7	122	2 S06823	Ig heavy chain V r
36	468.5	35.6	112	2 E30538	Ig kappa chain V r
37	468.5	35.6	112	2 F30538	Ig kappa chain V r
38	468	35.6	116	2 S15672	Ig heavy chain V r
39	467.5	35.6	113	2 UC2270	Ig heavy chain V r
40	467.5	35.6	118	2 S25174	PL7-6 antibody lig
41	467	35.5	112	2 S49220	Ig heavy chain V r
42	466	35.4	112	2 S09970	Ig gamma-1 chain -
43	465	35.4	97	2 A42575	Ig kappa chain V-J
44	464	35.3	133	1 K4HUT	Ig kappa chain V r
45	463.5	35.2	113	2 S30520	Ig kappa chain pre

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C/Accession: A56446

R/Jang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

U. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally den

A/Reference number: A56446; PMID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TAN>

A/Cross-references: GB:U20617

C/Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 65.2%; Score 857; DB 2; Length 268;
Matches 167; Conservative 26; Mismatches 45; Indels 12; Gaps 3;

QY	1 QVTLQSGAEIVRSGASVNLCTASGFNFKDYVMHWKORPERGLWMIGYIDSEGETTEV 60	
DB	3 QVTLQSGAEIVRSGASVNLCTASGFNFKDYVMHWKORPERGLWMIGYIDSEGETTEV 62	
QY	61 APNFGKATVADTSSNTAVYHLSSLTSEDVTYYCNNAVYYEDGVALDYWGQGTIVV 120	
DB	63 DKPFQKATVADTSSNTAVYHLSSLTSEDVTYYCNNAVYYEDGVALDYWGQGTIVV 118	
QY	121 SSGGGSGGGSGGGSDLELTPSPSLAVSAGEKXAMCKSSQSLFNSRTRKNYLAAYQ 180	
DB	119 SSGGGSGGGSGGGSDLELTPSPSLAVSAGEKXAMCKSSQSLFNSRTRKNYLAAYQ 171	
QY	181 QKPGSPKVLVMASTRESGVDPDRFGSSGSDFTLTSSVOAEDIAVYCKOSYMLP-T 239	
DB	172 QKSDASPKLVYITSLTPGVARRSGSSGSGNSYLTSSMESEDAITTCQFTSSPFT 231	
QY	240 FGGGTLEIK 249	
DB	232 FGGGTLEIK 241	

RESULT 2

S41374
single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C/Accession: S41374

R/Araenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antio

A/Reference number: S41374

A;Accession: S41374
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <ART>
A;Cross-references: EMBL:Z294800

Query Match	65.0%	Score	854.5	DB 2	length	249	
Best Local Similarity	68.3%	Pred	No. 1.4e-53				
Matches 1/2, Conservative	23	Mismatches	48	Indels	9	Gaps	4

```

QY      1  CYKQAESGAEIVRRSGASVNLSTASGFENIKDYIMHWKORPEEGELMIIGTIDESGTEY  60
Db      1  QVQLQSGSGEIVRRPGASVKLTSTASGFENFDYDIHWKORPEEGELMIARITAPASGVKY  60
QY      61  AENPGKALVWVADTSSNTSYHLHSILTSEDTYYYC--NAVIVKEYDGVRLADYWGQSTY  118
Db      1  VRFQDKATITDTSNTSYHLISLTSEDTIANYCARNDTLX-----TSIGWGQGSTV  115

```

2y 119 TVSSGGGGGGGGGGGGGGGGGGDIETQSPSSLVASAGEKAMSKSKSQTSPNSRFRKNYIAW 178
 116 TVSSKGGGGGGGGGGGGGGGGGGDIETQSPSPVAVIIGESVSIISCRSSKSLIYS-DGGDYLFW 174

QY 179 YQQKGGSPKLLIYMASTREGVDPDRPTGSGGTDFLLTISVSQAEDILAVYYCKOSYLP 238
: : : : :
Db 175 FLQRFGSPQLLTLYMSNLASCPDPRFSGSGGSTFTLIRISKVEAEIDVGVIYCMQHRRYP 234

QY	239	-TFGGTKLEIK	249
		:	
Db	235	LTFGAGTKLEIK	246

RESULT 3

p53 specific single-chain antibody Pab421 - human
C,Species: Homo sapiens (man)
C,Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997

A/Title: Characterization of scFv-421, a single-chain antibody targeted to p53

A/Accession: U75322
A/Molecule type: mRNA
A/Residues: 1-233 <JAN>

Query Match 64.0%; Score 841.5; DB 2; Length 233;
C;Comment: This protein specifically binds the tumor suppressor protein p53. It

	Matches	165;	Conservative	24;	Mismatches	44;	Indels	11;	Gaps	2							
QY	5	QESGALVVS	GASAVNLSCT	ASGENIKY	NWAMV	KOREEGL	EWLGYID	PSGREN	YAPNF	64							
Db	1	QESGALVVS	GASAVNLSCT	SGENIN	DIYHAWK	REGL	EWLGR	IDP	ENGDAD	MRSS	60						
QY	65	QKGATV	TADTSS	NTAVI	HLSS	LTSE	DTT	YVY	CNAV	IYEB	DGALD	YMG	QCT	ITV	VS	SGG	12

Db 61 GYKATMTADTSNTAYLTQSLTSEDYAVYYCA-----GMDYWGQTITVTSGG 11

QY 125 GSGSGGSGSGSDIELTQSPSLAVSAGEKVMASCKSSQSLFNSRTREKNYLIANYQQRG 18

Db 1.12 GSSGGSRAGGGSDIELTQSPASLAVSLGORATISCRASKSV--STSGSYSMENNQQRPG 16

Db 170 QPRLILYLVSNLBSGVAPRFSSGSGIDFTLNLHPVEEDDARYYCQHIRELIRSEGT 22
QY 245 KLEI 248

Db 230 KLEI 233

RESULT 4

S43103
Ig heavy chain V-H region (AB1 WT) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 24-May-2001
C:Accession: S43103
C:Collector: D.: Braud F.: Margaritte C.: Delpech A.: Tron, F.

submitted to the EMBL Data Library, March 1994
A:Description: An idotype D23-bearing polyclonal, murine anti-DNA monoclonal antibody
A:Reference number: S42484
A:Accession: S43103

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <GIL>
3;Accession: EMBL:J21353. NID:0467574. PIDD:CAAR3231 1: PIDD:0467575
3;Accession: EMBL:J21353. NID:0467574. PIDD:CAAR3231 1: PIDD:0467575

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match	41.4%;	Score 544;	DB 2;	Length 112;
Best Local Similarity	93.8%;	Pred. No. 5.4e-32;		
Matches 105; Conservative	3;	Mismatches 4;	Indels 0;	Gaps 0;

QY 138 DIETLSPSSSLAVSAGAEKVMASCKSSGQLFNSTRKNYLAMQQKPGDSPEKLIIWASTR 19
|| : || || || || || || || || || || || || || || || || || || || || || ||
Db 1 DIVMSQSPSSSLAVSAGEKVTMCKSSQSLLNSRTRKNYLAMQQKPGDSEKLLIYWASTR 60

QY 198 ESGVDFRFGSGSGDTFLTITSSVQAEADIAVYCKQSYNLETFGGGKLEIK 249
DB 61 ESGVDFRFGSGSGDTFLTITSSVQAEADIAVYCKQSYNLETFGGGKLEIK 112

RESULT 5

Ig light chain V region (S107/VH11 group 1-4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

U. Behar, S. M. Lustgarten, D. L. Corbett, S. Scharff, M. D. J. Exp. Med. 173, 731-741, 1991

A;Accession: P10407
A;Molecule type: DNA
A;Residues: 1-113 <BBH>

C;Keywords: immunoglobulin F;16-96/Domain: immunoglobulin homology <IMM>

```

Best Local Similarity 92.9%; Pred. No. 1.5e-31;
Matches 104; Conservative 3; Mismatches 5; Indels 0; Gaps 0

```

1 DIVISOSPSLAVSAGEKVTMSCKSSQSLNSRTIRNYIAYQOKGQSPKLLIYNASTR 60

Db 61 ECGVDFRTGGSGTDFTLTISVQAEADLAVYYCKQSNLYTFGGGKLEIK 11

RESULT

Ig kappa chain V region (anti-DNA, DP13VK and DP18VK) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000

R. Shlomchik, M. Mascelli, M. Shan, H. Radic, M. Z. Piserksy, D. Marshak-Rothstein, U. Exp. Med. 171, 265-297, 1990

U. Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A;Accession: P10265
A;Molecule type: mRNA

```

A;Residues: 1-112 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-96/Domain: immunoglobulin homology <IMM>
F;24-40/Region: complementarity-determining 1
F;41-55/Region: framework 2
F;56-62/Region: complementarity-determining 2
F;63-94/Region: framework 3
F;95-102/Region: complementarity-determining 3
F;103-112/Region: framework 4

Query Match      40.5%; Score 533; DB 2; Length 112;
Best Local Similarity 92.0%; Pred. No. 3.3e-31;
Matches 103; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      138 DIETSPSSILASAGEKVMSCSKSSQLFNSTRRTKNYLAWYQKPGOSPKVLIYWASTR 197
        ||::|||
Db       1 DVMGSPSSLAVSAGKVTMSCKSSQSLEFSRRKNVLAWYQKPGOSPKLLIYWASTR 60

QY      138 ESGVPDRFTGGSGGTDFTLTITSSVQAEDLAIVYYCKQSYNLPTFGGCTKLEIK 249
        ||::|||
Db       61 ESGVPDRFTGGSGGTDFTLTITSSVQAEDLAIVYYCKQSYNLPTFGGCTKLEIK 112

RESULT 7
PS0023      Ig kappa chain precursor V region (6A4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jul-1990 #text_change 21-Jan-2000
C;Accession: PS0023
R;Margut, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Gene 74, 335-345, 1988
A>Title: Cloning and characterization of cDNAs coding for the heavy and light chains of
A;Reference number: PS0023; MUID:89232725; PMID:3149944
A;Accession: PS0023
A:Molecule type: mRNA
A;Residues: 1-133 <MAR>
A;Experimental source: strain BALB/c
A>Note: The amino-terminal four residues of the mature protein were directly sequenced
C;Comment: This chain was obtained from a monoclonal antibody against Pseudomonas aeruginosa
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-133/Product: Ig kappa chain V region 6A4 #status experimental <IGV>
F;36-116/Domain: immunoglobulin homology <IMM>

Query Match      40.5%; Score 533; DB 2; Length 133;
Best Local Similarity 89.7%; Pred. No. 3.9e-31;
Matches 104; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY      134 GGGSDELTQSPSSILASAGEKVMSCSKSSQLFNSTRRTKNYLAWYQKPGOSPKVLIYW 193
        ||::|||
Db       17 GTGCDIVMSGSPSSLAVSAGEKVTMSCKSSQSLSLRKNFLAWYQKPGOSPKLLIYW 76

QY      194 ASTRESGVDPDRFTGGSGGTDFTLTITSSVQAEDLAIVYYCKQSYNLPTFGGCTKLEIK 249
        ||::|||
Db       77 ASTRESGVDPDRFTGGSGGTDFTLTITSSVQAEDLAIVYYCKQSYNLPTFGGCTKLEIK 132

RESULT 8
PT0408      Ig light chain V region (SI07/VH11 group 1-6) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PT0408
J;Behar, S.M.; Lustgarten, D.L.; Corbet, S.; Scharff, M.D.
U. Exp. Med. 173, 733-741, 1991
A>Title: Characterization of somatically mutated SI07 VH11-encoded anti-DNA autoantibody
A;Reference number: PT0376; MUID:91147903; PMID:1900082
A;Accession: PT0408
A:Molecule type: DNA
A;Residues: 1-113 <BEH>
```

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C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match          39.5%; Score 520; DB 2; Length 113;
Best Local Similarity 90.2%; Pred. No. 2,7e-30;
Matches 101; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY      138 DIETQSPSSLAIVSAGEKVMSCKSSQSLFNSRTRKNYLAWVQKQSPKVLITYMASTR 197
      |||:::|||||
Db       1 DIVMSQSPSSLAIVSAGEKVTWMSCKSSQSLNSRTRKNYLAWVQKQSPKVLITYMASTR 60

QY      198 ESGVPDRFTSGSGSDFTLTITSSVQAEIDLAIVYCKQSYNLPTFGGGTKLEIK 249
      |||:::|||||
Db       61 ECGVPDRFTSGSGSDFTLTITSSVQAEIDLAIVYCKQSYNLPTFGGXTLFLFX 112

RESULT 9
S41393
Ig kappa chain V region (12.5H VL) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Mar-2001
C:Accession: S41393
R:Margartite, C.; Gilbert, D.; Brard, F.; Tron, F.
submitted to the EMBL Data Library, January 1994
A:Description: Structural characterization of an (NZB X NZM) F1 mouse-derived IGM anti-1
A:Reference number: S41393
A:Accession: S41393
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <MAR>
A:Cross-references: EMBL:Z29536
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match          39.1%; Score 514; DB 2; Length 112;
Best Local Similarity 88.4%; Pred. No. 7.2e-30;
Matches 99; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY      138 DIETQSPSSLAIVSAGEKVMSCKSSQSLFNSRTRKNYLAWVQKQSPKVLITYMASTR 197
      |||:::|||||
Db       1 DIVMSQSPSSLAIVSAGEKVTWMSCKSSQSLNSRTRKNYLAWVQKQSPKVLITYMASTR 60

QY      198 ESGVPDRFTSGSGSDFTLTITSSVQAEIDLAIVYCKQSYNLPTFGGGTKLEIK 249
      |||:::|||||
Db       61 DSGVPDRFTSGSGSDFTLTITSSVQAEIDLAIVYCKQSYNLPTFGGGTKLEIK 112

RESULT 10
S03304
Ig kappa chain V region (61B8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C:Accession: S03304; J00043
R:Van Cleave, V.H.; Naeye, C.W.; Metzger, D.W.
J. Exp. Med. 167, 1841-1848, 1988
A>Title: Do antibodies recognize amino acid side chains of protein antigens independent
A:Reference number: J10043; WTID:88258372; PMID:2455014
A:Accession: S03304
A:Molecule type: mRNA
A:Residues: 1-111 <VAN>
A:Cross-references: EMBL:X12380; NID:g52341; PIDN:CA30938.1; PID:g930189
A>Note: the authors translated the codon GAT for residue 76 as Asn
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match          38.3%; Score 503.5; DB 2; Length 111;
Best Local Similarity 89.2%; Pred. No. 4e-29;
Matches 99; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY      138 DIETQSPSSLAIVSAGEKVMSCKSSQSLFNSRTRKNYLAWVQKQSPKVLITYMASTR 197

```

Db 1 DIVTOSPSLSIAVSAEKKTLTCKSSQILNSTRKNYLAWYQKRGSPKLIYMASTR 60

QY 198 ESGVDPDRFTGSGSGTDFTLTSSVQAEADLAIVYCKOSYNLP-TFGSGTKLE 247
 Db 61 ESGVDPDRFTGSGSGTDFTLTSSVQAEADLAIVYCKOSYNLP-TFGSGTKLE 111

RESULT 11

S04576

Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
 C/Accession: S04576

R/Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.; TH
 Eur. J. Immunol. 17, 91-95, 1987

A>Title: Molecular analysis of the murine lupus-associated anti-self response: involvement
 A/Reference number: S04573; MUID:87133856; PMID:3102255

A/Accession: S04576
 A/Molecule type: mRNA

A/Residues: 1-136 <KOF>

A/Cross-references: EMBL:X14624; NID:g52029; PID:CAA32777.1; PID:g52030

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterodimer; immunoglobulin

F/1-19/Domain: signal sequence #status predicted <SIG>
 F/20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 38.1%; Score 501.5; DB 2; Length 136;
 Best Local Similarity 77.0%; Pred. No. 6.9e-29;
 Matches 94; Conservative 11; Mismatches 12; Indels 5; Gaps 1;

QY 1 QVKLESGSEIVRSAGSVNLCTASGFNKKDYMMWVKRPREGLEWIGYIDPESGETRY 60
 Db 20 EYVLQOQSGELVRPGASVNLCTASGFNKKDYMMWVKRPREGLEWIGYIDPESGETRY 79

QY 61 APNFOGKATVTAADTSNTAYLHLSITSEDTVYVCNAVITYEYDGYALDYWGQGTTVV 120
 Db 80 ASKFGKKNMTADTSNTAYLQLSITSEDTAVYYCTT-----YKAYMDYWGQGTSTTV 134

QY 121 SS 122
 Db 135 SS 136

RESULT 12

PH1101
 Ig light chain V region (clone 111.19) - mouse

C/Species: Mus musculus (house mouse)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C/Accession: PH1101

R/Tillman, D.M.; Jon, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992

A>Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1101

A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA

A/Residues: 1-104 <TIL>

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F/16-96/Domain: immunoglobulin homology <IMM>

Query Match 37.9%; Score 498; DB 2; Length 104;
 Best Local Similarity 92.3%; Pred. No. 9e-29;
 Matches 96; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 138 DIELTQSPSSSLAVSAGEKVMSCSSQSLFNSRTRKNYLAWYQKRGSPKLIYMASTR 197
 Db 1 DIVTOSPSLSIAVSAEKKTLTCKSSQILNSTRKNYLAWYQKRGSPKLIYMASTR 60

QY 198 ESGVDPDRFTGSGSGTDFTLTSSVQAEADLAIVYCKOSYNLP-TFG 241

Db 61 ESGVDPDRFTGSGSGTDFTLTSSVQAEADLAIVYCKOSYNLP-TFG 104

RESULT 13

PH1047

Ig light chain V region (clones 165.45 and 163.c1) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C/Accession: PH1047; PH1049

R/Tillman, D.M.; Jon, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992

A>Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1047

A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA

A/Residues: 1-103 <TIL>

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F/16-96/Domain: immunoglobulin homology <IMM>

Query Match 37.8%; Score 497; DB 2; Length 103;
 Best Local Similarity 93.2%; Pred. No. 1e-28;
 Matches 96; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 138 DIELTQSPSSSLAVSAGEKVMSCSSQSLFNSRTRKNYLAWYQKRGSPKLIYMASTR 197
 Db 1 DIVTOSPSLSIAVSAEKKTLTCKSSQILNSTRKNYLAWYQKRGSPKLIYMASTR 60

QY 198 ESGVDPDRFTGSGSGTDFTLTSSVQAEADLAIVYCKOSYNLP-TFG 240
 Db 61 ESGVDPDRFTGSGSGTDFTLTSSVQAEADLAIVYCKOSYNLP-TFG 103

RESULT 14
 PH1102
 Ig light chain V region (clone 111.61) - mouse

C/Species: Mus musculus (house mouse)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C/Accession: PH1102

R/Tillman, D.M.; Jon, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992

A>Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
 A/Reference number: PH0971; MUID:92381444; PMID:1512540

A/Accession: PH1102

A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA

A/Residues: 1-104 <TIL>

A/Experimental source: B cell, strain [NZB x NZW]F1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: immunoglobulin

F/16-96/Domain: immunoglobulin homology <IMM>

Query Match 37.8%; Score 497; DB 2; Length 104;
 Best Local Similarity 91.3%; Pred. No. 1.1e-28;
 Matches 95; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 138 DIELTQSPSSSLAVSAGEKVMSCSSQSLFNSRTRKNYLAWYQKRGSPKLIYMASTR 197
 Db 1 DIVTOSPSLSIAVSAEKKTLTCKSSQILNSTRKNYLAWYQKRGSPKLIYMASTR 60

QY 198 ESGVDPDRFTGSGSGTDFTLTSSVQAEADLAIVYCKOSYNLP-TFG 241
 Db 61 ESGVDPDRFTGSGSGTDFTLTSSVQAEADLAIVYCKOSYNLP-TFG 104

RESULT 15

PH1051

Ig light chain V region (clone 165.3) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PH1051
 R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
 A:Reference number: PH0971; MUID:92381444; PMID:1512540
 A:Accession: PH1051
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-103 <TIL>
 A:Experimental source: B cell, strain [NZB x NZW]F1
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 37.4%; Score 492; DB 2; Length 103;
 Best local similarity 92.2%; Pred. No. 2.4e-28;
 Matches 95; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 138 DIELTQSPSSLAVSAGEKVMSCSKSSOSLFNSRTKRYLIAMYOQKPGQSEKVIITYMASTR 197
 Db 1 DIVMSQSPSSLAVSAGEKVMSCSKSSOSLFNSRTKRYLIAMYOQKPGQSEKVIITYMASTR 60
 QY 198 ESGVPDRFTSGSGCTDFTLTISVQAEIDIAVYCKQSYNLPTF 240
 Db 61 ESGVPDRFTSGSGCTDFTLTISVQAEIDIAVYCKQSYNLPTF 103

Search completed: July 30, 2004, 11:21:46
 Job time : 13.6646 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 30, 2004, 11:15:41 ; Search time 8.09756 Seconds

(without alignments)
1601.157 Million cell updates/sec

Title: US-09-297-181-4

Perfect score: 1315

Sequence: 1 QVKQESGAEIVRSGASVNL.....YCKQSYNLPTFGGTXLEIK 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	464	35.3	133	KVAB_HUMAN	P06313 homo sapien
2	463.5	35.2	134	KVAC_HUMAN	P06314 homo sapien
3	448.5	34.1	114	KV4A_HUMAN	P01625 homo sapien
4	418	31.8	121	KV4D_HUMAN	P83593 homo sapien
5	405.5	30.8	109	KV4D_HUMAN	P01751 mus musculu
6	400	30.4	139	HV07_MOUSE	P01751 mus musculu
7	393.5	29.9	114	KV1A_MOUSE	P01632 mus musculu
8	393.5	29.9	120	HV03_MOUSE	P01747 mus musculu
9	380.5	28.9	149	KV5B_MOUSE	P01633 mus musculu
10	378.5	28.8	136	HV11_MOUSE	P01755 mus musculu
11	378	28.7	137	HV11_MOUSE	P01746 mus musculu
12	376.5	28.6	140	HV02_MOUSE	P01746 mus musculu
13	371.5	28.6	121	HV01_MOUSE	P04431 homo sapien
14	371.5	28.3	129	KV1M_HUMAN	P01605 homo sapien
15	369.5	28.1	108	KV1M_HUMAN	P01600 homo sapien
16	367.5	27.9	108	KV1M_HUMAN	P01744 homo sapien
17	366	27.8	147	KV1Y_HUMAN	P80362 homo sapien
18	365.5	27.8	108	KV1Y_HUMAN	P01664 mus musculu
19	365.5	27.8	111	KV3L_MOUSE	P01624 mus musculu
20	365.5	27.8	117	HV12_MOUSE	P01624 mus musculu
21	363	27.6	109	KV3F_HUMAN	P18135 homo sapien
22	362	27.5	129	KV3L_HUMAN	P04430 homo sapien
23	361.5	27.5	108	KV1Y_HUMAN	P01670 mus musculu
24	361.5	27.5	111	KV3R_MOUSE	P01620 mus musculu
25	361	27.5	109	KV3B_HUMAN	P01620 mus musculu
26	361	27.5	109	KV3D_HUMAN	P01620 mus musculu
27	361	27.5	113	KV2G_MOUSE	P01631 mus musculu
28	360	27.4	117	KV2G_HUMAN	P06309 mus musculu
29	359.5	27.3	117	HV13_MOUSE	P01757 mus musculu
30	359	27.3	120	HV50_MOUSE	P06329 mus musculu
31	358.5	27.3	111	KV3U_MOUSE	P01673 mus musculu
32	357	27.1	129	KV3H_HUMAN	P04207 homo sapien
33	357	27.1	129	KV3M_HUMAN	P18136 homo sapien

34	356.5	27.1	115	1	KV2A_HUMAN	P01614 homo sapien
35	355	27.0	108	1	KV3A_HUMAN	P01672 homo sapien
36	354.5	27.0	111	1	KV3T_MOUSE	P01672 mus musculu
37	354.5	27.0	138	1	HV4B_MOUSE	P03980 mus musculu
38	354	26.9	107	1	KV1D_HUMAN	P01596 mus musculu
39	354	26.9	110	1	KV3P_MOUSE	P01668 mus musculu
40	353.5	26.9	111	1	KV3S_MOUSE	P01671 mus musculu
41	353	26.8	118	1	HV51_MOUSE	P06330 mus musculu
42	352.5	26.8	108	1	KV1P_HUMAN	P01608 homo sapien
43	352.5	26.8	108	1	KV5P_MOUSE	P01649 mus musculu
44	352.5	26.8	111	1	KV3Q_MOUSE	P01667 mus musculu
45	352	26.8	109	1	KV3E_HUMAN	P01623 homo sapien

ALIGNMENTS

Query Match	Score	DB 1;	Length
Best Local Similarity	75.0%;	Pred. No. 4e-28;	
Query Match	35.3%;	Score 464;	DB 1; Length 133;
Best Local Similarity	75.0%;	Pred. No. 4e-28;	

Matches 87; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

QY 134 GGGSDIELTQSPSSLAIVSAGEKVMSCKSQSLFNSRTKNTLYAWYQKPGQSPKYLITW 193
 DB 17 GAYGDIWMTQSPDLSLAIVSAGEKATINCKSSQSLVSNKNTLYAWYQKPGQPKLITW 76

QY 194 ASTRESGVDRPRTGSGGTDFLTITSSVQAEIDLAVYCKQSYNLPTRGGGTLEIK 249
 DB 77 ASTRESGVDRPRTGSGGTDFLTITSSVQAEIDLAVYCKQSYNLPTRGGGTLEIK 132

RESULT 2
 KY4C_HUMAN STANDARD; PRT; 134 AA.
 AC P06314;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-IV region B17 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041854; PubMed=2997713;
 RA Marsh P., Mills F., Gould H.;
 RT "Detection of a unique human V kappa IV germline gene by a cloned
 RT cDNA probe."
 RL Nucleic Acids Res. 13:6531-6544(1985).
 RN [2]
 RA Marsh P.;
 RT REVISION TO 76.
 RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.

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DR EMBL: X02990; CAA26733.1; -
 DR HSSP: P80362; 1MTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART; SM00406; IGV, 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL
 FT CHAIN 1 134 IG KAPPA CHAIN V-IV REGION B17.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 61 75 FRAMEWORK-2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 83 114 FRAMEWORK-3.
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 122 133 FRAMEWORK-4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 134
 SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 35.2%; Score 463.5; DB 1; Length 134;
 Best Local Similarity 76.1%; Pred. No. 4.4e-28;
 Matches 89; Conservative 11; Mismatches 16; Indels 1; Gaps 1;

QY 134 GGGSDIELTQSPSSLAIVSAGEKVMSCKSQSLFNSRTKNTLYAWYQKPGQSPKYLITW 193
 DB 17 GAYGDIWMTQSPDLSLAIVSAGEKATINCKSSQSLVSNKNTLYAWYQKPGQPKLITW 76

DB 17 GAYGDIWMTQSPDLSLAIVSAGEKATINCKSSQSLVSNKNTLYAWYQKPGQPKLITW 76

QY 194 ASTRESGVDRPRTGSGGTDFLTITSSVQAEIDLAVYCKQSYNLPTRGGGTLEIK 249
 DB 77 ASTRESGVDRPRTGSGGTDFLTITSSVQAEIDLAVYCKQSYNLPTRGGGTLEIK 133

RESULT 3
 KY4A_HUMAN STANDARD; PRT; 114 AA.
 AC P01625;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-IV region Len.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76004342; PubMed=50995;
 RA Schneider M., Hilschmann N.;
 RT "The primary structure of a monoclonic immunoglobulin-L-chain of
 RT subgroup IV of the kappa type (Bence-Jones protein Len)."
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
 RN [2]
 RP REVISION TO 9.
 RA Salomon A.;
 RT Submitted (AUG-1986) to Swiss-Prot.
 CC -1- MISCELLANEOUS: THIS C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.

DR PDB; 1BEQ; 01-FEB-01.
 DR PDB; 1BEU; 03-FEB-01.
 DR PDB; 1BEQ; 09-FEB-01.
 DR PDB; 1EK3; 06-MAR-01.
 DR PDB; 1LVE; 21-JAN-98.
 DR PDB; 3LVE; 18-MAY-99.
 DR PDB; 5LVE; 28-MAR-01.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART; SM00406; IGV, 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
 KW DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 41 55 FRAMEWORK-2.
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 63 94 FRAMEWORK-3.
 FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 102 113 FRAMEWORK-4.
 FT DISULFID 23 94 BY SIMILARITY.
 FT NON_TER 114
 SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 34.1%; Score 448.5; DB 1; Length 114;
 Best Local Similarity 76.1%; Pred. No. 4.8e-27;
 Matches 86; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 138 DIELTQSPSSLAIVSAGEKVMSCKSQSLFNSRTKNTLYAWYQKPGQSPKYLITWASTR 197
 DB 1 DIVMTQSPDLSLAIVSAGEKATINCKSSQSLVSNKNTLYAWYQKPGQPKLITWASTR 60

QY 198 ESGVDRPRTGSGGTDFLTITSSVQAEIDLAVYCKQSYNLPTRGGGTLEIK 249
 DB 61 ESGVDRPRTGSGGTDFLTITSSVQAEIDLAVYCKQSYNLPTRGGGTLEIK 113

RESULT 4

KV40 HUMAN STANDARD; PRT; 121 AA.
 ID KV40 HUMAN
 AC P06312;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ig kappa chain V-IV region precursor (Fragment).
 GN IGKV4-1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86041853; PubMed=2997712;
 RA Klobbeck H.G., Bornkamm G.W., Combiato G., Mocikat R., Pohlenz H.D.,
 RA Zachau H.G.;
 RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
 RT single germline gene."
 RL Nucleic Acids Res. 13:6515-6529(1985).
 CC -1- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
 CC -----
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 CC -----
 DR EMBL; Z00023; CAA7318.1; -;
 DR PIR; A01902; K4HU.
 DR HSSP; P80362; 1WTL.
 DR Genew; HSC5834; IGKV4-1.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003596; IG_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 >121 IG KAPPA CHAIN V-IV REGION.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 61 75 FRAMEWORK-2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 83 114 FRAMEWORK-3.
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;
 Query Match 31.8%; Score 418; DB 1; Length 121;
 Best Local Similarity 74.3%; Pred. No. 9.6e-25;
 Matches 78; Conservative 11; Mismatches 16; Indels 0; Gaps 0;
 QY 134 GGGSDIEITQSPSSLAIVSNGEKVAMSCKSSQSLFNSRRKKNYLAAYQQKPGSPKVLTYW 193
 DB 17 GAYGIVMTQSPDLSAVLSGERATINCKSSQSVLVSSNNKNYLAAYQQKPGSPKVLTYW 76
 QY 194 ASTRESGVPRDRTGSGSGTDFLTITSSVOAEDLAAYYCKQSNLP 238
 DB 77 ASTRESGVPRDRTGSGSGTDFLTITSSVOAEDLAAYYCKQSNLP 121
 RESULT 5
 ID KV4D HUMAN STANDARD; PRT; 109 AA.
 AC P83593;
 DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-IV region SRH (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Abdominal adipose tissue;
 RX MEDLINE=98249779; PubMed=9588180.
 RA Olsen K.E., Sletten K., Westermarck P.;
 RT "Extended analysis of AL-amyloid protein from abdominal wall
 RT subcutaneous fat biopsys: kappa IV immunoglobulin light chain."
 RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
 CC -1- FUNCTION: May play an important role in fibrillogenesis.
 CC InterPro: IPR007110; IG-like.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR003596; IG_v.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00409; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 41 55 FRAMEWORK-2.
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 63 94 FRAMEWORK-3.
 FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 102 109 FRAMEWORK-4.
 FT DISULFID 23 94 BY SIMILARITY.
 FT UNSURE 23 23
 FT UNSURE 94 94
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 12060 MW; 0C4F31E11E12A0B CRC64;
 Query Match 30.8%; Score 405.5; DB 1; Length 109;
 Best Local Similarity 69.7%; Pred. No. 7.3e-24;
 Matches 76; Conservative 13; Mismatches 19; Indels 1; Gaps 1;
 QY 138 DIEITQSPSSLAIVSNGEKVAMSCKSSQSLFNSRRKKNYLAAYQQKPGSPKVLTYW 197
 DB 1 DIWVTQSPDLSAVLSGERATINCKSSQSVLVSSNNKNYLAAYQQKPGSPKVLTYW 60
 QY 198 ESGVPRDRTGSGSGTDFLTITSSVOAEDLAAYYCKQSNLP-TFGGGRK 245
 DB 61 ESGVPRDRTGSGSGTDFLTITTPGLOAEDVAAYYCKQYRIRYTPGQAK 109
 RESULT 6
 ID HV07 MOUSE STANDARD; PRT; 139 AA.
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region B1-8/186-2 precursor.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Botwell A.L.M., Paskind M., Reth M., Tanishii-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NPb family of
 RT antibodies: somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THE B1-8 MT CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL

```
CC (NRP ANTIBODIES).
CC -----
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CC -----
CC EMBL; J00529; AAA38170.1; -.
CC DR PIR; A90809; MEMS18.
CC DR PDB; 1A6U; 27-MAY-98.
CC DR PDB; 1A6W; 15-JUL-98.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG_LIKE; 1.
CC KM Immunoglobulin V region; Signal; 3D-structure.
CC FT SIGNAL 1 19
CC FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
CC FT DOMAIN 20 49 FRAMEWORK-1.
CC FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 55 68 FRAMEWORK-2.
CC FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 86 117 FRAMEWORK-3.
CC FT DOMAIN 118 124 D SEGMENT.
CC FT DOMAIN 125 139 JH2 SEGMENT.
CC FT DISULFID 41 115 BY SIMILARITY.
CC FT NON TER 139 139
CC SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

Query Match 30.4%; Score 400; DB 1; Length 139;
Best Local Similarity 63.4%; Pred. No. 2.5e-23;
Matches 78; Conservative 14; Mismatches 27; Indels 4; Gaps 2;

QY 1 OVKLQSSGAEIVRSAGSVNLSTAGSFNFKDYMMWVKRPREGLEWIGYIDPESSETRY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 QVLOQDPGAEIVKPGASVNLSTAGSYFTSYMMWVKRPRGLEWIGRIDPNSGGTRY 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 AHNFOGKATVATDTSNTAYLHLSITSEDTVYYCNNAVYYEYDGYA-LDYWGQGVTV 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NKKFKSKATLVYDKPSSTAYMQLSITSEDSAVYYC--ARDYVGSSTFDYWGQGVTV 136
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 120 VSS 122
   |||
Db 137 VSS 139
   |||

RESULT 7
KVIA MOUSE STANDARD; PRT; 114 AA.
ID KVIA_MOUSE STANDARD; PRT; 114 AA.
AC P01632;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region S107A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8141357; PubMed=6788890;
RA Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;
RT "Nucleic acid and protein sequences of phosphocholine-binding light
RT chains";
RL J. Exp. Med. 153:1366-1370(1981).

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CC -----
CC EMBL; U29423; AAC00033.1; -.
CC DR PIR; A01915; KMS37A.
CC DR HSSP; P01607; IRE1.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG_LIKE; 1.
CC KM Immunoglobulin V region.
CC FT DOMAIN 1 23 FRAMEWORK-1.
CC FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
CC FT DOMAIN 41 55 FRAMEWORK-2.
CC FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
CC FT DOMAIN 63 94 FRAMEWORK-3.
CC FT DOMAIN 95 103 COMPLEMENTARITY-DETERMINING-3.
CC FT DOMAIN 104 113 FRAMEWORK-4.
CC FT DISULFID 23 94 BY SIMILARITY.
CC FT NON TER 114 114
CC SQ SEQUENCE 114 AA; 12717 MW; 32008BC89DB367B CRC64;

Query Match 29.9%; Score 393.5; DB 1; Length 114;
Best Local Similarity 68.1%; Pred. No. 6e-23;
Matches 77; Conservative 16; Mismatches 19; Indels 1; Gaps 1;

QY 138 DIETLOSPSPSLAVSGEKVMSCKSSQSLFNERTKKNYAVYQKPGSPKLYIWASTR 197
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 DVTWQSPFTFLAVYASKKTVTISCTASSTSYSSKHKVHYIAMYQKPEQSPKLYIGASNR 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 198 ESGVDPDRFTGSGSGDTFTLLTSSVQAEPLAVYYCKQSYNLP-TFGGKTLRLK 249
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 YGVVDPRFTGSGSGDTFTLLTSSVQAEPLAVYYCKQSYNLP-TFGGKTLRLK 113
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
HV03 MOUSE STANDARD; PRT; 120 AA.
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8131846; PubMed=6186498;
RA Siekevitz M., Gelfer M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idioType response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -I- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIAL GENE THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT. JH2.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSSP; P01789; IMCP.
CC DR InterPro; IPR007110; Ig-like.
CC DR InterPro; IPR003596; Ig_v.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00406; IGV; 1.
CC DR PROSITE; PS50835; IG_LIKE; 1.
CC KM Immunoglobulin V region; Hydrindoma.
CC FT DOMAIN 1 111 IG-LIKE.
CC FT NON TER 120 120
CC SQ SEQUENCE 120 AA; 13307 MW; FFO4E4A167B654AF CRC64;
```

Query Match 29.9%; Score 393.5; DB 1; Length 120;
 Best Local Similarity 60.3%; Pred. No. 6.4e-23;
 Matches 73; Conservative 20; Mismatches 27; Indels 1; Gaps 1;

QY 2 VKLQESGAEIVRSASVNLSTAGSEINIKQYMMWVQREPEGLWIGYIDPESGETEYA 61
 Db 1 VQLQSGAEIVRSASVNLSTAGSEINIKQYMMWVQREPEGLWIGYIDPESGETEYA 61
 QY 62 PNFQKATVTADTSSNTAYLHLSLTSEDTVYVCNAVYYEYDGYALDYWGQGTVTVS 121
 Db 61 EKFQKATVTADTSSNTAYLHLSLTSEDTVYVCNAVYYEYDGYALDYWGQGTVTVS 119

QY 122 S 122
 Db 120 S 120

RESULT 9
 KVS5_MOUSE STANDARD; PRT; 149 AA.
 AC P01633;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-V region MFC11 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 [1]

RP SEQUENCE OF 1-71 FROM N.A.
 RX MEDLINE=83001944; PubMed=6288267;
 RA Kelley D.B., Coleclough C., Perry R.P.;
 RT "Functional significance and evolutionary development of the
 RL 5'-terminal regions of immunoglobulin variable-region genes.";
 RN Cell 29:681-689(1982).
 [2]

RP SEQUENCE OF 41-149 FROM N.A.
 RX MEDLINE=80176554; PubMed=6245773;
 RA Rabbits T.H., Hamlyn P.H., Matthysens G., Roe B.A.;
 RT "The variability, arrangement, and rearrangement of immunoglobulin
 RL genes.";
 RN Can. J. Biochem. 58:176-187(1980).
 [3]

RP SEQUENCE OF 30-149.
 RX MEDLINE=78186617; PubMed=418775;
 RA Smith G.P.;
 RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
 RL myeloma MPC 11.";
 RN Biochem. J. 171:337-347(1978).
 [4]

CC -I- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
 CC AMINO END. DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
 CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
 CC RESIDUE OF TYPICAL KAPPA CHAINS.
 CC -----
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 CC -----
 CC EMBL; J00561; AAA38776.1; -
 CC PIR; A90823; KVM511.
 CC HSSP; P80362; IWTU.
 CC InterPro; IPR007110; Ig_1like.
 CC InterPro; IPR003596; Ig_V.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00406; IGV; 1.
 CC PROSITE; PSS0835; IG_LIKE; 1.
 CC Immunoglobulin V region; Signal; Repeat.
 KW

FT SIGNAL 1 29
 FT CHAIN 30 149 IG KAPPA CHAIN V-V REGION MFC11.
 FT DOMAIN 42 64 FRAMEWORK-1.
 FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 76 90 FRAMEWORK-2.
 FT DOMAIN 91 97 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 98 129 FRAMEWORK-3.
 FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 139 148 FRAMEWORK-4.
 FT REPEAT 26 35
 FT REPEAT 38 47
 FT NON TER 149 149
 SQ SEQUENCE 149 AA; 16434 MM; B0480C87B682AC3E CRC64;

Query Match 28.9%; Score 380.5; DB 1; Length 149;
 Best Local Similarity 65.0%; Pred. No. 7.6e-22;
 Matches 76; Conservative 16; Mismatches 18; Indels 7; Gaps 2;

QY 134 GGGSDIELTQSPSSLAIVSAGEKVMSCSKSOSLFNRTKNTIAYVQKPGSPKLTITW 193
 Db 38 GVDGDIWMTQSHKFMSTVGDVRSITCKASQDVSTT-----VAVYQKPGSPKLTITW 91

QY 194 ASTRESGVDPDRFTGSGSGTDFLTITSSVQAEPLAVYCKQSYNL-PTFGGKTLK 249
 Db 92 ASYRTYGVDPDRFTGSGSGTDFLTITSSVQAEPLAVYCKQHYSTPPTFGGKTLK 148

RESULT 10
 KVS5_MOUSE STANDARD; PRT; 136 AA.
 AC P01634;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain V-V region MOPC 21 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=82059477; PubMed=6170937;
 RA Hamlyn P.H., Galt M.J., Milstein C.;
 RT "Complete sequence of an immunoglobulin mRNA using specific priming
 RL and the dideoxynucleotide method of RNA sequencing.";
 RN Nucleic Acids Res. 9:4485-4494(1981).
 [2]

RP SEQUENCE OF 30-136.
 RX MEDLINE=73053310; PubMed=4638343;
 RA Svasti J., Milstein C.;
 RT "The complete amino acid sequence of a mouse kappa light chain.";
 RN Biochem. J. 128:427-444(1972).
 [3]

CC -I- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
 CC AMINO END. DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
 CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
 CC RESIDUE OF TYPICAL KAPPA CHAINS.
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 CC -----
 CC EMBL; V00810; CAA24192.1; ALU_TERM.
 CC PIR; A93736; KVM521.
 CC PDB; 1IGC; 03-JUN-95.
 CC InterPro; IPR007110; Ig_1like.
 CC InterPro; IPR003596; Ig_V.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00406; IGV; 1.
 CC PROSITE; PSS0835; IG_LIKE; 1.
 CC Immunoglobulin V region; Signal; 3D-structure.
 KW
 FT SIGNAL 1 29
 FT CHAIN 30 136 IG KAPPA CHAIN V-V REGION MOPC 21.
 FT DOMAIN 30 52 FRAMEWORK-1.

Query Match	Best Local Similarity	Score	DB 1	Length	136;
Matches 74;	Conservative 18;	Mismatches 18;	Indels 7;	Gaps 2;	
FT DOMAIN	53	63	COMPLEMENTARITY-DETERMINING-1.		
FT DOMAIN	64	78	FRAMEWORK-2.		
FT DOMAIN	79	85	COMPLEMENTARITY-DETERMINING-2.		
FT DOMAIN	86	117	FRAMEWORK-3.		
FT DOMAIN	118	126	COMPLEMENTARITY-DETERMINING-3.		
FT DOMAIN	127	136	FRAMEWORK-4.		
FT NON TER	136	136			
SEQUENCE	136 AA;	14902 MW;	BCDD85113996D1C2 CRC64;		
Query Match	28.8%;	Score 378.5;	DB 1;	Length 136;	
Best Local Similarity	63.2%;	Pred. No. 9.6e-22;			
Matches 74;	Conservative 18;	Mismatches 18;	Indels 7;	Gaps 2;	
QY	134	GGGSDILDTGPPSSSLAYSAGKVMGSKSSQSLFNSTRKNTYLAAMVQKKGSPKYLIV	193		
DB	26	GADNINVTQSPKSMSSVGERVLTICKASENV-----TYSWVQKREGSPKILLIG	79		
QY	194	ASTRESGVPDPSFTSGSGTGTFTLTITSSVQADIAVYCKSYNLP-TFGGTYLEIK	249		
DB	80	ASNRYTGVPDPFTSGSGATDFTLTITSSVQADLADYHCGGYSPYPTGGGTYLEIK	136		
RESULT 11					
HV11_MOUSE	STANDARD;	PRT;	137 AA.		
ID HV11_MOUSE	20175;				
AC	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig heavy chain V region S43 precursor.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_TaxID=10090;					
SEQUENCE FROM N.A.					
RA	MEDLINE=61234548; PubMed=6788376;				
RA	Bottomwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,				
RA	Baltimore D.;				
RT	"Heavy chain variable region contribution to the Npb family of				
RT	antibodies: somatic mutation evident in a gamma 2a variable region.";				
RL	Cell 24:625-637(1981).				
CC	-1- MISCBLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA				
CC	MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL				
CC	(NPB ANTIBODIDS).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; J00539; AAA38172.1; -				
DR	PIR; A02038; G2MG43.				
DR	HSP; P01810; 2FBU.				
DR	InterPro; IPR007110; IG_1like.				
DR	InterPro; IPR003596; IG_V.				
DR	Pfam; PF00047; IG_1.				
DR	SMART; SM00406; IGV_1.				
DR	PROSITE; PS50835; IG_LIKE_1.				
KW	Immunoglobulin V region; Signal.				
FT SIGNAL	1	137			
FT CHAIN	20	137	IG HEAVY CHAIN V REGION S43.		
FT DOMAIN	20	49	FRAMEWORK-1.		
FT DOMAIN	50	54	COMPLEMENTARITY-DETERMINING-1.		
FT DOMAIN	55	68	FRAMEWORK-2.		
FT DOMAIN	69	85	COMPLEMENTARITY-DETERMINING-2.		
FT DOMAIN	86	117	FRAMEWORK-3.		
FT DOMAIN	118	122	D SEGMENT.		
FT DOMAIN	123	137	JH2 SEGMENT.		
FT DISULFID	41	115	BY SIMILARITY.		

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FT   NON TER      137       137
SQ   SEQUENCE    137 AA; 15200 MW; ADD5881BF44B8BC9 CRC64;

Query Match          28.7%; Score 378; DB 1; Length 137;
Best Local Similarity 61.5%; Pred. No. 1, le-21;
Matches              75; Conservative 11; Mismatches 32; Indels 4; Gaps 2;

QY   1 QVKLSEGAIVTSASVNI..SCTASGFN1KDYMMWVKORPEEGHWTIGTIDPESGETFY 60
     |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB   20 QVOIQGAGAFVPFGASVYKSKSCASGYTFLSYMHWNRPGSGLEWIGRIDPNISGGTTY 79
     :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY   61 APNFQKAIVTADTSSNTAYLAHLSSLTSETTYYYGNVAIYYEYDGDALDWGGGTLYTV 120
     ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB   80 NEHPRKATLTITDKPSSTAYMOLSLTSEDSAVYVC---AFRYLGRT-FDIWGQTTLTV 135
     |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY   121 SS 122
     |||
DB   136 SS 137

RESULT 12
HV02_MOUSE STANDARD; PRT; 140 AA.
ID HV02_MOUSE
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 93G7 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RC MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RT Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
-----
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CC CC -----
DR EMBL; J00493; AAA38128.1; -
DR PIR; A94264; HVMSG7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig_-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; ig_1.
DR SMART; SM00406; Igv_1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hydrioma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query March          28.6%; Score 376.5; DB 1; Length 140;
Best Local Similarity 58.2%; Pred. No. 1, 4e-21;
Matches              71; Conservative 13; Mismatches 31; Indels 1; Gaps 1;

QY   1 QVKLSEGAIVTSASVNI..SCTASGFN1KDYMMWVKORPEEGHWTIGTIDPESGETFY 60
     |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB   20 EVGIQGAGAEIVRAGSVVKKMSCKASGYTFETSYGINWVKORPGGGLWIGINPDNGNYIN 79
     :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
```

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QY 61 APNFGKATVADTSSNTAYHLSSLTSEDTVVYCNNAVITYEYDGYALDYMGGTIVTV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 NEKKKGKTTTLVDKSSSTAYWQALSLTSEDSAVYFCARSHRYG-GSYDFYWGQGTTLTV 138

QY 121 SS 122
   |||
Db 139 SS 140

RESULT 13
HVO1_MOUSE STANDARD; PRT; 121 AA.
ID HVO1_MOUSE
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MPC11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MELOMA THAT SECRETES IGG2B.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A93708; GWSM11.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON TER 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 28.6%; Score 375.5; DB 1; Length 121;
Best Local Similarity 59.0%; Pred. No. 1.4e-21;
Matches 72; Conservative 18; Mismatches 31; Indels 1; Gaps 1;

QY 1 QVKIQSGAELVRSAGSYNLSTASGPNIKDYHMYKOREEGLEMTGYIDPSGGETY 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EAOLQOSGAELVRSAGSYNLSTASGPNIKDYHMYKOREEGLEMTGYIDPSGGETY 60

QY 61 APNFGKATVADTSSNTAYHLSSLTSEDTVVYCNNAVITYEYDGYALDYMGGTIVTV 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 NDNLKGRATLTADTSSSTAYVQLSSLTSEDSATYHCARGIYNSSPY-FDSWGQGTTLTV 119

QY 121 SS 122
   |||
Db 120 SS 121

RESULT 14
KVIM_HUMAN STANDARD; PRT; 129 AA.
ID KVIM_HUMAN
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.

```

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC -----
DR EMBL; X00965; GAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUMK.
DR HSSP; P01607; IRET.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; F:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2P9 CRC64;

Query Match 28.3%; Score 371.5; DB 1; Length 129;
Best Local Similarity 62.4%; Pred. No. 3e-21;
Matches 73; Conservative 20; Mismatches 17; Indels 7; Gaps 2;

QY 134 GGSGLDILTPSSSLAVSAGEKYAMSCSSQSLFNSRTRKNYILAMYQKPGQSPKVLITYW 193
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 19 GARDIDIGMTQSPSSLSASVGRVITTCRASGI-----SYLAWMYQKPKAPKAPLILYA 72

QY 194 ASTRESGVDPRTFGSSGSDFTLTITSSVQAEIDLAVYCKQSYN-LPTFGGTYKLEIK 249
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 73 ASLSQSGVTSRFSGSGSDFTLTITSSLOPEDSATYVCOQSYSTLTITGGQTRLEIK 129

RESULT 15
KVIM_HUMAN STANDARD; PRT; 108 AA.
ID KVIM_HUMAN
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;

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RA  Capra J.D., Klapper D.G.;
RT  "Complete amino acid sequence of the variable domains of two human
RT  IgM anti-gamma globulins (Iay/Pom) with shared idiotypic
RT  specificities."
RL  Scand. J. Immunol. 5:677-684(1976).
CC  -1- MISCELLANEOUS; THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC  CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC  WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC  -1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC  GLOBULIN ACTIVITY.
DR  PIR; A01871; K1H0LY.
DR  HSP; P01607; 1REI.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; IG-like.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IGV; 1.
DR  PROSITE; PS50835; IG LIKE; 1.
KW  Immunoglobulin V region.
FT  DOMAIN 1 23
FT  DOMAIN 24 34 FRAMEWORK-1.
FT  DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN 50 56 FRAMEWORK-2.
FT  DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 89 97 FRAMEWORK-3.
FT  DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT  DISULFID 23 88 FRAMEWORK-4.
FT  NON TER 108 108 BY SIMILARITY.
SQ  SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 28.1%; Score 369.5; DB 1; Length 108;
Best Local Similarity 62.8%; Pred. No. 3,5e-21;
Matches 71; Conservative 20; Mismatches 15; Indels 7; Gaps 2;

QY 138 DIELTQSSPSLAVSAGEKAMSCSKSSQSLFNSRTRKNYLAAYQOKKQSPKLIYMASTR 197
DB 1 DIQMTQSSPSLAVSYGDRVTITCOASQNV-----NATLNMVQOKKGLAPKLIYGASTR 54

QY 198 ESGVDPDRFTGSGSGTDFTLTITSSVQAEIDLAVYCKQSYNL-PTFGGTRLEIK 249
DB 55 EAGVSRFRSGSGSGTDFTTITSSLQPDIALFYCCQYNNWNPPTFGGTRKVEVK 107

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Search completed: July 30, 2004, 11:19:47
 Job time : 9.09756 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 30, 2004, 11:16:06 ; Search time 35.4268 Seconds
(without alignments)
2217.642 Million cell updates/sec

Title: US-09-297-181-4
Perfect score: 1315
Sequence: 1 QVKLQSGAGELVRSASVNL.....YCKQSYNLPTFGGKLEIK 249

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	800	60.8	243	11 Q7QM2	Q7QM2 mus musculus
2	744.5	56.6	298	11 Q9QYF0	Q9QYF0 mus musculus
3	713	54.2	241	11 Q921A6	Q921A6 mus musculus
4	613	46.6	218	11 Q925B1	Q925B1 mus musculus
5	493	37.5	468	11 Q99L31	Q99L31 mus musculus
6	441	33.5	170	11 Q925S2	Q925S2 mus musculus
7	436.5	33.2	107	11 Q9ER29	Q9ER29 mus musculus
8	433.5	33.0	109	11 Q9UL85	Q9UL85 mus musculus
9	420.5	32.0	146	11 Q924Q3	Q924Q3 mus musculus
10	416	31.6	145	11 Q924R4	Q924R4 mus musculus
11	414.5	31.5	473	11 Q99L25	Q99L25 mus musculus
12	412	31.3	145	11 Q924R1	Q924R1 mus musculus
13	411	31.3	488	11 Q8K0F2	Q8K0F2 mus musculus
14	408	31.0	145	11 Q924Q9	Q924Q9 mus musculus
15	406.5	30.9	146	11 Q924R8	Q924R8 mus musculus
16	406	30.9	145	11 Q924Q6	Q924Q6 mus musculus

17	403	30.6	145	11 Q924P7	Q924P7 mus musculus
18	403	30.6	482	11 Q8K172	Q8K172 mus musculus
19	402	30.6	143	11 Q924R0	Q924R0 mus musculus
20	400	30.4	143	11 Q924P9	Q924P9 mus musculus
21	400	30.4	145	11 Q924Q7	Q924Q7 mus musculus
22	400	30.4	473	11 Q9D8L4	Q9D8L4 mus musculus
23	399.5	30.4	23	11 Q924R2	Q924R2 mus musculus
24	397	30.2	143	11 Q91V67	Q91V67 mus musculus
25	395	30.0	143	11 Q924Q5	Q924Q5 mus musculus
26	392.5	29.8	463	11 Q99L04	Q99L04 mus musculus
27	392	29.8	613	11 Q8VCX7	Q8VCX7 mus musculus
28	390	29.7	141	11 Q924Q4	Q924Q4 mus musculus
29	389	29.6	145	11 Q924R3	Q924R3 mus musculus
30	388.5	29.5	481	11 Q91WT1	Q91WT1 mus musculus
31	387	29.4	107	4 Q96S49	Q96S49 homo sapien
32	387	29.4	137	11 Q924R6	Q924R6 mus musculus
33	385.5	29.3	142	11 Q924Q1	Q924Q1 mus musculus
34	384	29.2	118	11 Q921C4	Q921C4 mus musculus
35	383.5	29.2	144	11 Q924P5	Q924P5 mus musculus
36	383	29.1	143	11 Q924R7	Q924R7 mus musculus
37	382.5	29.1	142	11 Q924Q2	Q924Q2 mus musculus
38	380	28.9	143	11 Q924P6	Q924P6 mus musculus
39	379.5	28.9	117	11 Q9QX9	Q9QX9 mus musculus
40	379.5	28.9	278	11 Q921K1	Q921K1 mus musculus
41	379	28.8	470	11 Q7TWK1	Q7TWK1 mus musculus
42	378.5	28.8	146	11 Q924Q8	Q924Q8 mus musculus
43	378	28.7	143	11 Q91VA2	Q91VA2 mus musculus
44	377	28.7	238	11 Q8VC16	Q8VC16 mus musculus
45	377	28.7	239	11 Q8VC55	Q8VC55 mus musculus

ALIGNMENTS

RESULT 1					
Q7QM2	PRELIMINARY;	PRT;	243 AA.		
ID	Q7QM2				
AC	Q7QM2				
DT	01-OCT-2003 (TREMblrel. 25, Created)				
DT	01-OCT-2003 (TREMblrel. 25, Last sequence update)				
DT	01-OCT-2003 (TREMblrel. 25, Last annotation update)				
DE	ScFv 6H8 protein (Fragment).				
OS	ScFv 6H8.				
GN	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Balb/C;				
RA	Peter J C, Eftekhari P, Billiard P, Wallukat G;				
RT	"scFv single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor."				
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AJ574851; CAE00495.1; -				
FT	NOM TER				
FT	1				
FT	1				
SO	SEQUENCE	243 AA;	25976 MW;	BEFF64D2DC4F76 CRC64;	
QY	Query Match	60.8%;	Score 800;	DB 11;	Length 243;
QY	Best local Similarity	61.0%;	Pred. No. 2.7e-57;		
QY	Matches 152;	Conservative 38;	Mismatches 47;	Indels 12;	Gaps 2;
Db	1	QVKLQSGAGELVRSASVNLCTASGFNIDYWMWKORPEGLWNTGYDPPSGETEV	60		
QY	1	QVKLQSGAGELVRSASVNLCTASGFNIDYWMWKORPEGLWNTGYDPPSGETEV	120		
Db	61	AFNFGKATVADTSTNTAYLHLSLTSEDTTYYCAVAYYEXDGYALDYGGQTTVT	114		
QY	61	AFNFGKATVADTSTNTAYLHLSLTSEDTTYYCAVAYYEXDGYALDYGGQTTVT	120		
Db	121	SSGGGSGGGGSGGGGSDIEITQSPSSLAASAGKVMASCKSSQSLNSRRKMYLAMYQ	180		
QY	121	SSGGGSGGGGSGGGGSDIEITQSPSSLAASAGKVMASCKSSQSLNSRRKMYLAMYQ	180		
Db	115	SSGGGSGGGGSGGGGSDIOWTQSSSFSVSLGDRVITTCASSEDYNR-----LAWYQ	168		
QY	115	SSGGGSGGGGSGGGGSDIOWTQSSSFSVSLGDRVITTCASSEDYNR-----LAWYQ	168		

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QY 181 QKPGSPKVLIVWASTRESGVPDRFTSGSGGTDTLTTISSVQAEPLAVYCKQSYNLPF 240
DB 169 QKPGVAPRLTISGATSLTGVPSRPSGSGKDYLTSLTQTEADVATYCCQVWSTWTF 228
QY 241 GGGTKLEIK 249
DB 229 GGGTKLEIK 237

RESULT 2
QOYF0 PRELIMINARY; PRT; 298 AA.
AC QOYF0;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE CN 8 scfv.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phage display subtraction
RT method.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAAB8633.1; -.
DR PIR; A33933; A33933.
DR PIR; S19112; S19112.
DR HSSP; P01607; 1REI.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 56.6%; Score 744.5; DB 11; Length 298;
Best Local Similarity 56.4%; Pred. No. 1.2e-52;
Matches 141; Conservative 37; Mismatches 61; Indels 11; Gaps 3;

QY 1 QVKLOESGAEIVRSASVNLCTASGFNIKDYMHVWQRPBEGLEWIGYIDPESGETEY 60
DB 40 QVKLOSGGGLVYKPGSLKLSCAASGDFSRVWMSWVQAPQKGLFWIGELNPDSGLNY 99
QY 61 APNPGKATVTADTSSNTAYVHLSLTSEDVTYVCNAVITYEYGYALDWGGSTVTV 120
DB 100 TPLSLDKRTTISRDNANKNTLYLQMSKVRSEDTALYYCARASYGHSA---YWGQGTIVTV 155
QY 121 SSGGGSGGGSGGGSGDIETLQSPSSLAVSAGEKVMSCSSQSLFNSRRTKXNYAYO 180
DB 156 SSGGGSGGGSGGGSGDIETLQSPSSLASVAGEVITVITTCASGNI-----HNYLAYO 209
QY 181 QKPGSPKVLIVWASTRESGVPDRFTSGSGGTDTLTTISSVQAEPLAVYCKQSYNLP 239
DB 210 QKQKSPQLLVYNAKTLADGVPSRPSGSGGTQYSLKINSIQPEDFGSYVCOHFWTPTPT 269
QY 240 FGGTKLEIK 249
DB 270 FGGTKLEIK 279

RESULT 3
Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TREMblrel. 19, Created)

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DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.-J., Kim I.-J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scfv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 241 AA; 26086 MW; 02768872489C771 CRC64;

Query Match 54.2%; Score 713; DB 11; Length 241;
Best Local Similarity 53.8%; Pred. No. 3.3e-50;
Matches 136; Conservative 44; Mismatches 55; Indels 18; Gaps 4;

QY 1 QVKLOESGAEIVRSASVNLCTASGFNIKDYMHVWQRPBEGLEWIGYIDPESGETEY 60
DB 1 QVKLOSGPELKKGETYKISCKASGYFTTLYGMWVQVQAKGLKMWGMINTYIGERTY 60
QY 61 APNPGKATVTADTSSNTAYVHLSLTSEDVTYVCNAVITYEYDGYALDWGGSTVTV 120
DB 61 ADDEKGRPAFLFLEMSASTAYVQINNKKEDTATYFCARKDLRY---FDYWGQGTIVTV 116
QY 121 SSGGGSGGGSGGGSGDIETLQSPSSLAVSAGEKVMSCSSQSLFNSRRTKXNYAYO 180
DB 117 SSGGGSGGGSGGGSGDIETLQSPSSLASVAGEVITVITTCASGDI-----NKXIAYO 170
QY 181 QKPGSPK---VLIVWASTRESGVPDRFTSGSGGTDTLTTISSVQAEPLAVYCKQSYN 236
DB 171 HKPGKSPSALTHTY----IQPGLPSRPSGSGSDYSPSISNLEPPDIATYVGLHVDN 226
QY 237 LPTFGGTKLEIK 249
DB 227 LHTFGGTKLEIK 239

RESULT 4
Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
[2]

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AC Q9ER29;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti human TNF-alpha light chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-hTNF-a monoclonal antibody."
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RT human TNF-alpha specific monoclonal antibody."
RL T1 4 Chun 1 Ta Hsueh Hsueh Pao 19:373-376(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF262753; AAC23804.1; -.
DR PDB; 2AP2; 24-NOV-99.
DR PDB; 2AC9; 24-JUL-02.
DR PDB; 43CA; 24-JUL-02.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match 33.2%; Score 436.5; DB 11; Length 107;
Best Local Similarity 77.6%; Pred. No. 3.9e-28;
Matches 83; Conservative 12; Mismatches 11; Indels 1; Gaps 1;

QY 141 LTGSPSSIAVAGAKVAMSCSSQSLSFRRKRYLAWYQKPGQSPKVLITYMASTPESG 200
DB 1 MTQSPSSIAVAGAKVAMSCSSQSLSNTQKYLAWYQKPGQSPKVLITYMASTPESG 60

QY 201 VPDRTSGSGCTDEFTLTITSSVQADLAVYYCKQSNLP-TEGGGSKL 246
DB 61 VPDRTSGSGCTDEFTLTITSSVQTEDLADYFCQCHYRTPFTGSGTKL 107

RESULT 8
Q9JL85 PRELIMINARY; PRT; 109 AA.
ID Q9JL85;
AC Q9JL85;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-myosin immunoglobulin heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALB/c;
RC MEDLINE=20448942; PubMed=1092488;
RX Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206021; AAF69319.1; -.

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DR HSSP; P01810; 2FBT.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 109 AA; 11944 MW; DFE615FE6CD4DE CRC64;

Query Match 33.0%; Score 433.5; DB 11; Length 109;
Best Local Similarity 70.9%; Pred. No. 6.9e-28;
Matches 83; Conservative 11; Mismatches 12; Indels 11; Gaps 2;

QY 9 AELVRCASVNLCTASGFNIKQYHMYVQRPBEGLEMGYIDPESGETEYAPNPGKA 68
DB 1 AELVRCASVNLCTASGFNIKQYHMYVQRPBEGLEMGYIDPESGETEYAPNPGKA 60

QY 69 TWTADTSSNTAVYHLSTLSEDTTVYYC--NAVYYEYDGYALDYGCGTTVSS 122
DB 61 TITSDTSSNTAVYQLSSTLSEDTAVYYCYRGAIVF-----DYGCGTALTVSS 109

RESULT 9
Q924Q3 PRELIMINARY; PRT; 146 AA.
ID Q924Q3;
AC Q924Q3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6;
RC Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067797; BAB63282.1; -.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1

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PT NON TER 146 146
SQ SEQUENCE 146 AA; 16136 MM; CEABDD6E1955807F CRC64;
Query Match 32.0%; Score 420.5; DB 11; Length 146;
Best Local Similarity 65.6%; Pred. No. 1.2e-26;
Matches 80; Conservative 14; Mismatches 27; Indels 1; Gaps 1;
QY 1 QVQLQESGAEIVRSGASVNLSTASGPNIKDYMMHWKQRPREGLEWIGYIDPESGETEY 60
Db 1 QVQLQPGAEIVRPGASVNLSTASGAYTTSYMMHWKQRPREGLEWIGYIDPESGETEY 60
QY 61 APNFGKATVYADTSSNTAYLHLSLTSEDTTYTCNAVIYYEYDGYALDYWGQGTIVY 120
Db 61 NEKFQKATLVTKPSSTAYMQSLSTSDSAVYTC-ARSLYDGYDYMADYWGQGTISVTV 119
QY 121 SS 122
Db 120 SS 121
RESULT 10
Q924R4 PRELIMINARY; PRT; 145 AA.
ID Q924R4;
AC 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE VHL6.2-D-U-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-nitrophenyl)Acetyl (NP).";
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067785; BAB63270.1; -
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 145 AA; 16081 MM; ECD0A135E05B8AA CRC64;

Query Match 31.6%; Score 416; DB 11; Length 145;
Best Local Similarity 66.4%; Pred. No. 2.7e-26;
Matches 81; Conservative 14; Mismatches 25; Indels 2; Gaps 2;
QY 1 QVQLQESGAEIVRSGASVNLSTASGPNIKDYMMHWKQRPREGLEWIGYIDPESGETEY 60
Db 1 QVQLQPGAEIVRPGASVNLSTASGAYTTSYMMHWKQRPREGLEWIGYIDPESGETEY 60
QY 61 APNFGKATVYADTSSNTAYLHLSLTSEDTTYTCNAVIYYEYDGYALDYWGQGTIVY 120
Db 61 NEKFQKATLVTKPSSTAYMQSLSTSDSAVYTC-ARSDYD-YADYWGQGTISVTV 118
QY 121 SS 122
Db 119 SS 120
RESULT 11
Q99L25 PRELIMINARY; PRT; 473 AA.
ID Q99L25;
AC 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 1810060009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IGMHC; 1.
SQ SEQUENCE 473 AA; 52449 MM; BE9889B7986DA155 CRC64;

Query Match 31.5%; Score 414.5; DB 11; Length 473;
Best Local Similarity 38.1%; Pred. No. 1.6e-25;
Matches 101; Conservative 35; Mismatches 68; Indels 61; Gaps 8;
QY 1 QVQLQESGAEIVRSGASVNLSTASGPNIKDYMMHWKQRPREGLEWIGYIDPESGETEY 60
Db 20 QVQLQPGAEIVRPGASVNLSTASGAYTTSYMMHWKQRPREGLEWIGYIDPESGETEY 79
QY 61 APNFGKATVYADTSSNTAYLHLSLTSEDTTYTCNAVIYYEYDGYALDYWGQGTIV 118
Db 80 NEKFQKATLVTKPSSTAYMQSLSTSDSAVYTC-ARSDYD-YADYWGQGTISVTV 139
QY 119 TVSSGGGGSGGGSGGGSDIELTQSPSLAV-----SAGEKAMSKCKSSQS;FNKTR 172
Db 140 TVSSA-----KTTAPSYVPLAPVCGDTTSSVTLGC-----LV 172
QY 173 KNYLAWYQKPGQSPKYLIVASFRSGV-----PDRTSGSGSGDFTLTSSVQAE 224
Db 173 KGYF-----PEPTLLTNSSGSLSSGVTFFPAVLQSDLYTLSSS---VTVTSSTWFSQ 221
QY 225 DIAVYYCKGSGYNLEPTFGGFKLBIK 249
Db 222 SI-----TCNVAHPASSTKVDKK 239
RESULT 12
Q924R1 PRELIMINARY; PRT; 145 AA.
ID Q924R1;
AC Q924R1;

DR PIR; PH1128; PH1128.
 DR PIR; PH1129; PH1129.
 DR PIR; PH1131; PH1131.
 DR PIR; PH1137; PH1134.
 DR PIR; PH1137; PH1137.
 DR PIR; PH1139; PH1139.
 DR PIR; PH1142; PH1142.
 DR PIR; PH1144; PH1144.
 DR PIR; PH1147; PH1147.
 DR PIR; PH1149; PH1149.
 DR PIR; PH1150; PH1150.
 DR PIR; PH1151; PH1151.
 DR PIR; PH1152; PH1152.
 DR PIR; PH1153; PH1153.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 145
 SQ SEQUENCE 145 AA; 16001 MW; 0F409EB09FA333D2 CRC64;

Query Match 31.0%; Score 408; DB 11; Length 145;
 Best Local Similarity 63.9%; Pred. No. 1.2e-25;
 Matches 78; Conservative 14; Mismatches 28; Indels 2; Gaps 1;

QY 1 QVQLQSGAEIVYSGASVNI SCTASGFNFKDYMHVWVWVORPEGLFWMIGYIDPESGETEY 60
 1 QVQLQSGAEIVYSGASVNI SCTASGFNFKDYMHVWVWVORPEGLFWMIGYIDPESGETEY 60
 Db
 QY 61 APNFGKATVYADTSSNTAYLHLSITSEDTTVYVCNAVYYEYDGYALDYMVGQGTITVY 120
 61 NEKFKSKATLVTKPKSPSTAYMQLSITSEDSAVYYCARSLITY--YANDYMGQGSITVY 118
 Db
 QY 121 SS 122
 119 SS 120

RESULT 15
 ID Q924R8 PRELIMINARY; PRT; 146 AA.
 AC Q924R8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE VHA166-2-D-J-C mu protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCB1_TaxID=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Kozono Y., Kozono H., Azuma T.;
 RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
 RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
 RT Hydroxy-3-Nitrophenyl)Acetyl (NP)";
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB067781; BAB63266.1; -.
 DR PIR; F28833; F28833.
 DR PIR; PH1105; PH1105.
 DR PIR; PH1108; PH1108.
 DR PIR; PH1114; PH1114.
 DR PIR; PH1118; PH1118.
 DR PIR; PH1119; PH1119.
 DR PIR; PH1125; PH1125.
 DR PIR; PH1126; PH1126.
 DR PIR; PH1128; PH1128.
 DR PIR; PH1129; PH1129.
 DR PIR; PH1131; PH1131.
 DR PIR; PH1134; PH1134.

DR PIR; PH1137; PH1137.
 DR PIR; PH1139; PH1139.
 DR PIR; PH1142; PH1142.
 DR PIR; PH1144; PH1144.
 DR PIR; PH1147; PH1147.
 DR PIR; PH1149; PH1149.
 DR PIR; PH1150; PH1150.
 DR PIR; PH1151; PH1151.
 DR PIR; PH1152; PH1152.
 DR PIR; PH1153; PH1153.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 146
 SQ SEQUENCE 146 AA; 16216 MW; 92460F1DFB7538 CRC64;

Query Match 30.9%; Score 406.5; DB 11; Length 146;
 Best Local Similarity 64.8%; Pred. No. 1.6e-25;
 Matches 79; Conservative 12; Mismatches 30; Indels 1; Gaps 1;

QY 1 QVQLQSGAEIVYSGASVNI SCTASGFNFKDYMHVWVWVORPEGLFWMIGYIDPESGETEY 60
 1 QVQLQSGAEIVYSGASVNI SCTASGFNFKDYMHVWVWVORPEGLFWMIGYIDPESGETEY 60
 Db
 QY 61 APNFGKATVYADTSSNTAYLHLSITSEDTTVYVCNAVYYEYDGYALDYMVGQGTITVY 120
 61 NEKFKSKATLVTKPKSPSTAYMQLSITSEDSAVYYC-ASYYGSSLYEYDYMVGQGTITVY 119
 Db
 QY 121 SS 122
 120 SS 121

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